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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on: June 11, 2003, 17:31:56 ; Search time 2436 Seconds Title: June 11, 2003, 17:31:56 ; Search time 2436 Seconds Title: June 13, 2003, 17:31:56 ; Search time 2436 Seconds (without alignments) 1003-09-308-397-1 Sequence: Jacquence: Jacquence	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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•	T'D	SPNEU19	AX19404	AF19793	AE00735	BD00368	AE00841	AR19375	AE00660	AE01416	AEO1008	AE00631	AE01310	AX43272		AP00318	AE00531		ECFABHD	AE00021	D90745	BSY1393	BS08000	AE00785	AB02197	AF04466		AX41652	AE01377	AL62726	AC02088	AL59617	AX41301	AL59198	BSU5943	AE01052	AE00254	ALIGNMENTS		r c	oniae clone G54,		ή 1	e e	s; Lactobacillale	5) ., Herrero,J	Σ
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	901 GTAGCACTTTAGAAAATAG 921 27378 GTAGCACTTTTAGAAAATAG 27398 SULT 2 194049 AX194049 AX194049 BESION AX194049 AX194049 AX194049 AX194049 AX194049 AX194049 AX194049	SOURCE Streptococcus pneumoniae ORGANISM Streptococcus pneumoniae Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. REFERENCE I (bases 1 to 921) AUTHORS Dougherty, T.G., Pucci, M.G., Dougherty, B.A., Davison, D.B., Bruccoleri, R.E. and Thanassi, J.A. TITLE Novel bacterial genes and proteins that are essential for cell viability and thair uses JOURNAL Patent: WO 0149721-A 30 12-UL-2001; Bristol-Myers Squibb Co. (US) Location/Qualifiers	246 a 246 a 100 Similarit 216; Conse 1 ATGACTAP	6 GATTTCTATGATTCGATTGTCAAAGAACGATTGATCGAGGGAGTCAGGTGCTC 6 GATTTCTATGATCAGATTGTCAAAGAAACGATTGATCGAGGGAGTCAGGTGCTC 7 GGTTATGATTATCGTTATCTCATCGATTGTAGGAACGATTGATCGAGCGAG
Francesco, M., Polissi, A., Buell, G., Feger, G., Garcia, E., Peitsch, M. and Garcia-Bustos, J.F. TITLE Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate JOURNAL Microb. Drug Resist. 7 (2), 99-125 (2001) MEDLINE 2133329 1443348 REFERENCE 2 (bases 1 to 111135) REFERENCE 2 (bases 1 to 111135) AUTHORS Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C., de Francesco, M., Buell, G., Feger, G., Garcia, E., Peitsch, M. and Garcia-Bustos, J.F. TITLE Direct Submission JOURNAL Submitted (31-677-2000) Research Department, Glaxo Wellcome, S.A., Severo Ochoa 2, 28760 Tres Cantos, SPAIN * This sequence will be replaced * This sequence will be replaced	* the accession number will be preserved. Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Survey and the second process of the second	ATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGG ATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGG GATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGT GATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGT GATTGTCAAAGAAAACGATTGATCGAGCGAGTCAGGT CATTGATACGGAAGAAAACAAACTCAATCAGACCGG CATCGATACGGAAGAAGACAAACTCAATCAGACCGCGCGCG	OY 181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTATC	Qy 361 GAAGCGGCTCCTGGTGACTCTGGCAAGTTCTCAATACGCCAGTAGAGGTC 420 Db 26838 GAAGCGGTTCTTGAAAAGTTCTCAATACGCCAGTAGAGGTC 26897 Qy 421 ATTGAAGAAGCTTCTGAAAAGTTCTCGAATACTCCAGCCAACTATAAC 480 Db 26898 ATTGAAGAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 26957 Qy 481 ACACCTGCACAAATGGTTGTGAACTTGAAGTGGTTGATCGAGCGGTTGAACTT 540 Db 26958 ACACCTGCAAATCGTCATTGCTGAGAAGTGGTTGATGAGCGGCTTGAACTT 27017 Qy 541 TTGCAAAAAGCTTTGCTGAGAAAGTGGTTGATGAGGGGGTTGAACTT 27017 Qy 541 TTGCAAGAAGCCAAACGCTTGATTGATGATTGATCACCC 600 Db 27018 TTGCAAGAAGCCAAACGCTTGATTCCTCTTAAGGTGCCCTTTCACACC 27077 Qy 601 GCTCTCCTTGAGCCTGAAAACCTTGATACCTCTTAAGGTGCAGGTACCTTTCACCC 27077 Qy 601 GCTCTCCTTGAGCCTAGAAACCTTGAAAACTTGAAAACTTTAAAGGTGCAGAAAGTTCAAGGTCCCTTTTCACACC 27077

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similarity to ACCD_ECOLI (43% identity)"
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Matches 916; Conserv
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                                                                                                                                                                                                       similarity
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5499. 5984
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subunit of acetyl-CoA carboxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AccC; by similarity to ACCC_ECOLI (53% identity)"
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IGR00531"
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                                                                                                                                                                                                                                                                                                                                                                                 3394 TITGITIAAAAAAATGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTA 3453
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Streptococcus.

1 (bases 1 to 12039)

Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D.,
Peterson,S., Heidelberg,J., DeBOy,R.T., Haft,D.H., Dodson,R.J.,
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Hickey,E.K., Holt,I.E., Loffus,B.J., Yang,F., Smith,H.O.,
Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and
Graser,C.M.

Complete genome sequence of a virulent isolate of Streptococcus
3154 GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA
                                                                                                                                                         GCTCAGCTCTTGACGCGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC
                                                                                                                                                                                                                                                                                                        3334 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
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                                                           GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGGAGACATT
                                                                                                     GATITITACTIGICCCCTAGICGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGACATI
                                                                                                                                                                                                                                                         ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Streptococcus pneumoniae TIGR4
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SIPEDKDKGFVGGFGGMLVLESLEHAERGATITAEVVGVGNTCDAYHTSFPHPEG
OGAIKAIKLALEEBAISPEQVAYVYAHGTFPANEKGESGALVAVLGKEVPVSSTKSF
TGHLLGAAGAVEAITTIEAMRHNFVPMTAGTSEVSDYIEANVVGGGLEKEIFVAISN
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'product="acetyl-CoA carboxylase, bitoin carboxyl carrier
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)KPAFVTVGDSVKKGOTLVIIEAMKVMNEIPAPKDGVVTEILVSNEEMVEFGKGLVRI
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/trans]_table=11
/product="acety1-CoA carboxylase, carboxyl transferase,
opera subunit"
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lpha subunit"
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product="(3R)-hydroxymyristoyl-(acyl-carrier-protein)
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7963. .8070
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                  Glimmer2; putative"
                                                                                                                                                                    Score 913; DB 1; L
Pred. No. 1.8e-239;
0; Mismatches 5;
/gene="SP0428"
/note="identified by
                                     /codon_start=1
/transl_table=
                                                                                                                                                                    Query Match
Best Local Similarity 99.5%;
Matches 916; Conservative
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Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S., DeHokfins,J.A., Alborn,W. Jr., Fritz,L., Fu,D.-J., Fuller,W., Geringer,C., Gilmour,R., Glass,J.S., Khoja,H., Kraft,A., Lagace,R.,

Gilmour,R., Glass,J.S., Khoja,H., Kraft,A., Lu,J., Matsushima,P., McAhren,S., McHenney,M., McLeaster,K., Mundy,C., Micas,T.I., Noris,F.H., O'Gara,M., Peery,R., Robertson,G.T., Rockey,P., Sun,P.H., M., Winkler,M.E., Yang,Y., Young-Bellido,M., Zhao,G., Zook,C., Baltz,R.H., Jaskunas,S.R., Rosteck,P.R. Jr., Skatrud,P.L. and Glass,J.I.

Genome of the bacterium Streptococcus pneumoniae strain R6

J. Bacteriol. 183 (19), 5709-5717 (2001)
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                                                                                                               421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
                                                                                                                                                                                                                         481 ACACCTGCACAAATCGTCATTGCTGGAGAGGTGGTTGCAGTTGATCGAGCGGTTGAACTT
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Streptococcus pneumoniae R6 section 34 of 184 of the complete
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Streptococcus pneumoniae R6
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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AE008418.1 GI:154
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KEYWORDS
SOURCE
ORGANISM
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MEDLINE
PUBMED
REFERENCE
AUTHORS
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BD003687

SOLYDUCLECTION POLYDUCLECTION OF Streptococcus pneumoniae and sequence.

BD003687

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SUP 2001501833-A/7.

Unidentified.

Unidentified.

Unidentified.

Unidentified

PR 30-001501833-A/7

PD 13-FEB-2001;

PD 13-FEB-2001

PR 31-OCT-1997 UP 1998520718

PR 31-OCT-1997 UP 1998520718

PR 31-OCT-1997 US 60/02960

PI CHARLES A KUNSCH,GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI PI UNION CRAIGE A ROSEN, PI PI PI UNION CRAIGE A ROSEN, PI PI UNION CRAIGE A ROSEN, PI PI PI UNION CRAIGE A ROSEN, PI PI PI PI UNION CRAIGE A ROSEN, PI PI PI PI UNION CRAIGE A ROSEN, PI PI PI UNION CRAIGE A ROSEN, PI PI PI UNION CRAIGE A ROSEN, PI PI PI UNION CRAIGE A R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICHABL FANNON, BRIAN A DOUGHERTY
CI2N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
C12N1/21,
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99.5%; Pred. No. 1.8e-239;
ive 0; Mismatches 5; Indels.
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1. .19702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref≈"taxon:32644"
4548 c 3728 g 5
                                                       1977
  921
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                                Topology: Linear;
Key
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PC C12N1;
PC C12N1;
PC C12N1;
PC C12N1;
CC Stranc
CC Topolo
FH KeY
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORIGIN
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BD003687/c
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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VSIPVIAAGGIIADGEGAAAGMLGABAVQVGTRFVVAKESNAHPNYKEKILKARDIDT
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GGSVMAGQIAGLAVSKEETAEEILKDLYYGAAKKIQEEBASRWTGVVRND"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Malonyl acyl carrier protein transacylase"
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LDFEDAVALVAKRGAYMEEAAPADSGKWVAVLNTPVEVIEEACQKASELGVYTPANYN
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FSDFTCPLVGNTBAAVMQKEDIAQLLTRQVKBPVRFYESIGVMQEAGISNFIEIGPGK
VLSGFVKKIDQTAHLAHVEDQASLVALLEK".
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301. = 48pr0380"
3021. .4681
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4875. .5606
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2954. .3928

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/codon start=1

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/EC min="
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                                                                                                                 Direct Submission
Submitted (27-JUL-2001) Infectious Diseases Research, Eli Lilly and
Company, Lilly Research Labs, Indianapolis, IN 46285-0438, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Enoy1-Coa hydratase II"
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QLAMTGEALTAEKALEWGLVYRVSEAEKLEKTREQLIKKLRRASSNSYAAIKKLVWES
QFKDWQGYATLEINLQKSLAQTEDFKEGVRAHSERRRPKFIGK"
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ISRTESTBDLATEVAKKLMAKAGITGEELDFIILATITPDSMMFSTAARVQANIGANK
ISRTESTBDLATEVAKKLMAKAGITGEELDFIILATITPDSMMFSTARVQANIGANK
ARFDLTAACSGFVPALSTABKFIASGRFGKGLUVGSETLSKAVDWSDRSTAVLGDG
AGGYLLEASESQEHFLASSLMSDGSRBSCLTYGHSGLHSPFSDDGSADSFLKMGRTVP
DFAIRDVAKSIKQTIDESFIEVTDLDYLLHQANDRILDKMARKIGVDRAKLPANMME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Conserved hypothetical protein"
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Norris, F.H., O'Gara, M., Peery, R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud, P.L.
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protein_id="AAK99181.1"
db_xref="GI:15457938"
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(19ene="spx0376"
143. .1577
/gene="spx0376"
/note="probable transcriptional regulator"

    10925
    organism="Streptococcus pneumoniae R6"

                                                                                                                                                                                                                                                                                                                                    / rpt family="BOX element"
/ rpt family="BOX element"
/ rpt type=dispersed
/ rpt unit=Box_CBA
                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:171101"
complement(122..233)
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codon start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="phaB"
'EC_number="4.2.1,17"
'note="Putative"
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transl_table=11
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/gene="fabH"
/note="spx0377"
1577. .2551
/gene="fabH"
/EC number="2,3.1
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trans1 table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="phaB"
/note="spr0375"
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trans1_table=1
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                                                                                                                                                                                                                                                                                          strain="R6"
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                                      GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGGAGACATT
                                                                                                            GCTCAGCTCTTGACGCGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC
                                                                                                                                               ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
                                                                                                                                                                            ATGCAAGAAGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
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Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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    /organism="Streptococcus pneumoniae"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 908.4; DB 6;
Pred. No. 2.9e-238;
0; Mismatches 6;
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Sequence 256 from Patent WO0149721.
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Best Local Similarity 99.3%;
Matches 912; Conservative
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KSINTACSSSNDAIGDAFRSIKFGFQDVMLVGGTEASITPFAIAGFQALTALSTTEDP
TRASIFPDFUSRNGFVWGGSGMLVLESELBHARFRGATILLAEVVGFGNTCDAYHYSPH
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DKPAFVTVGDSVKKGQTLV1IEAMKVNNBIPAPKDGVVTEILVSNEEMVBFGKGLVRI
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Pred. No. 4.8e-239;
); Mismatches 6;
                                                                                                                                                                                                                                                       'product="Biotin carboxyl
                                                                       ISNTFGFGGHNAVLAFKRWENR
                                                                                                                                                                                EC number="6.4.1.2"
                                                                                     6866 .7351
/gene="accB"
/note="spr0383"
6866 .7351
/gene="accB"
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|abel=spr0383
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/gene="fabz
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4 (Dases I to 10909)
5 (Paretti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H.G., Majar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Vuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.

Submitted (10-ARR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA

Location/Qualifiers
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Ferretti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.

Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
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                                                          AAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGAATCGAGCGGTTGAACTTTTGCAAGAAG
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                                  AAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTGCAAGAAG
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Streptococcus pyogenes M1 GAS
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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MI GAS strain SF370, section
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Streptococcus pyogenes M1
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                                                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases I to 1196)
Black, M.Terence., Hodgson, J.Edward., Knowles, D.Justin.Charles.,
Nicholas, R.Oakley. and Stodola, R.King.
                                                                                         ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
                                                                                                                ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
                                                                                                                                                                                                ACACCTGCACAAATCGTCATTGCTGGAGAGTGGTTGCAGTTGATCGAGCGGTTGAACTT
                                                                                                                                                                                                                                 TIGCAAGAAGCAGGIGCCAAACGCTTGAITCCTCTTAAGGIGTCAGGICCCTTTCACACC
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56.8%; Score 523.2; DB 6;
Best Local Similarity 99.1%; Pred. No. 1.6e-132;
Matches 547; Conservative 0; Mismatches 3;
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Location/Qualifiers
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Sequence 8 from patent US 6348328.
AR193756 GI:20240348
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/generalization and sequence of this ORF has hope and acterminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D groups been determined from a spot isolated by 2-D groups and a spot isolated by 2-D groups are recorphoresis from another strain of S. pyogenes. Hogan, D. A., Whitton, M. M., Rogers, J. and R. A. VanBogelen.
2000. Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins. Uppublished data; Best Blastp hit = pir||G69842 3-oxoacyl-|Gcyl-carrier proteins synthase (EC 2.3.1.41) - Bacillus subtilis synthase (EC 2.3.1.41) - Bacillus subtilis of 2.343488| emb|CAB12991.1| (29910) similar to 3-oxoacyl-acyl-carrier protein synthase [Bacillus subtilis] acyl-carrier protein synthase [Bacillus subtilis] (codon start=1 / transl_table=11 / transl_table=11 / product="putative beta-ketoacyl-ACP synthase II" / product="putative beta-ketoacyl-ACP synthase II" / product="putative beta-ketoacyl-ACP synthase II" / protein.id="hak:34492.1" / translation="hyperportyrycycrycyllatyraphymyngvarinyablis propertyr (ALPANCARIPERDRYSLYALYAAREAINHADLNIEMVARINGENCE)" wmw.nickologiaclaeleever.
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/gene="accB"
/note="Best Blastp hit = pir||C75558 acetyl-CoA
carboxylase, bitoin carboxyl carrier protein - Deinococcus
radiodurans (strain R1)
carp[64578|gb|AAF09708.1|AB001874.5 (AE001874) acetyl-CoA
carboxylase, bitoin carboxyl carrier protein [Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MDIREIQAALPHRYPMLLVDRVLEVSDDHIVAIKNVTINEPFFN
GHFPHYPVMPGVLIMEALAQTAGVLELSKEENKGKLVFYAGMDKVKFKKQVVPGDQLV
MTATFIKRRGTIAVVEARAEVDGKLAASGTLTFACGQ"
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NQEHAVPPQVQLVPNPTASEASSPASVKDVPVEEQPQAESFVAEGDIVESPLVGVAY
LAASPDKPPFVAVGDTVKKGQTLVIIEAMKVMNEVPAPCDGVITEILVSNEDVIEFGQ
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SIPPDKDWGPINGESGAWLLESLEHAQERGATITAEIVGVONTCORYHTSPNBEG
SLABRALHLALQEGGIBABAINYVVAHGTGTPANEKGESQAIVAVLGKDVPVSSTKSF
TGHLLGAAGAIBAITSAMRHNYVPWTAGTQALSEDIBANVIFGEGKETAINYAISN
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/BC_muber="1.1.1.100"
/note="The N-terminal amino acid sequence of this ORF
been determined from a spot isolated by 2-D gel
                                                                                                                                                                                                                                                                                                                                               product="putative beta-hydroxyacyl-ACP dehydratase"
protein_id="AAK34490.1"
db_xref="GI:13622801"
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                                                                                  /note="Best Blastp hit = dbj|BAB16042.1| (AB030883) similar to Bacillus subtilis hydroxymyristoyl-(acyl carrier protein) dehydratase [Streptococcus
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/transl_table=11
/producE=putative_biotoin
/protein_id="AAKA4491.1"
/db_xref="G1:13622802"
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complement(4101..5333)
/gene="fabf"
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/codon_start=1
/transl_table=11
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/note="SPy1747"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTDDVSRILKEARDQGRLTTLDYANLIFDDFMELHGDRHFSDDGA
IVGGLAYLAGQPVTVIGIQKGKNLQDNLARNFGQPNPEGYRKALRLMKQAEKFGRPVV
TFINTAGAPFGVGAERRGGGRAIAKNDIMEMSDLKVPIIAIIIGEGGSGGALALAVADQ
VWMLENTWAYULSPEGFSILMKDGSRATEAAELMKITAGELYKWGIVDRIIPEHGYF
SSEIVDIIKANLISOTTSLQAKPLDQLLDERYQRFRKY"
COMPLEMENT (909. 11775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trainiation="Malfrekoryirithnnslkgsvshnvpevpdelfakcpackhm
iykkolgjakicptcsynfrisaoreltitvdbgspoelfysjertpevoekt
iykkolgjakicptcsynfrisaoreltitvdbgspoelfysjertpevoekt
ivkvjettglheavltogkawnkeoktalamoselfnasmgrivydekttfeelfeen
levvifttpeptgesinglmghworkvsavkkrhsiamoelfyttilippttgevtasfa
megdiillaepqslvgfagrrviettvrenlpddforgkaeflodhgfvdaivkrtelrdk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel electrophoresis from another strain of S. pyggenes. Hogan, D. A., Whitton, M. M. Rogers, J. and R. A. VanBogelen. 2000. Two-dimensional gel electrophoresis map of streptococus pyogenes proteins. Unpublished data.; Best Blastp hit = pix | A65818 acetyl-CoA carboxylase (biotin carboxylase subunit) accC - Bacillus subtilis syl | A553486 | map | (D844365.1) | (D844355.1) | (259116) acetyl-CoA carboxylase subunit (biotin carboxylase subunit (Bacillus acct) | (D844365.1) | (289116) acetyl-CoA carboxylase subunit (Bacillus acct) | (B844365.1) | (B8441365.1) | (B848168 | map | (B8411365.1) | (B841118) | (B84118) | (B8418) | (B8418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /traislation="MPKKILIANRGEIAVRIIRAARELGISTVAVYSEADKEALHTIL
ADBAICIGPARSKESYLANMSVLSAAIVTGAQAIHPGRGFISENSKRATMCCEMNIKR
IGPSASVWDKWGDKINARSEMIKAGVPVIPGSGGEVVNAGEALAIANKIGYPVWLKAS
AGGGGKGIRKVETBADLEAARNAAGDEALGARGNGAMYLEKVIYPAHTEVQILGDAY
GNIIHLGERDCSLQRNNQKVLEESPSIAIGNTLRHEMGQAAVRAAEAVAXENAGTIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLDBDSEKFYFWEMNTRIQVEHPVTEFVTGVDIVKEQIKIAAGQPLAINQEDITITGH
AIECRINAENTAFNFAPSPGKITDLYMPSGGVGLRVDSAVYNGYAIPPYYDSMIAKII
VHGSNRFDALMKWQRALVELEIEGIITWTDPQLDLISDKRVIAGDYDTSFLMETFLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Best Blastp hit = sp|Q54776|ACCD_SYNP7
ACETYL-COBNZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNI
BETA (ACCASE BETA CHAIN) >gi|139985|gb|AAB82034.1|
(U5923)" carboxyltransferase beta subunit [Synechococcus
                                                                                                                                                                     = dbj|BAB06884.1| (AP001517)
carboxyltransferase alpha subunit
                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
/product="putative acetyl-CoA carboxylase alpha subunit"
/protein_id="1AAK34487.1"
/db_xref="GI:13622798"
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|trans] table=11
|product="putative acetyl-CoA carboxylase beta subunit"
|protein_id="AAK34488.1"
|db_xref="GI:13622799"
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/db_xref="GI:13622800"
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/gene="accC"
                                                                                                                                                            /noTe="Best Blastp hit
acetyl-CoA carboxylase
[Bacillus halodurans]"
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/gene="accC"
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complement (909, .1775)
                                    complement (142. .912)
                                                                              gene="accA"
EC_number="6.4.1.2"
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/gene="fabZ"
/note="SPy1746"
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'transT_table=
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DKSYYSKODDESFORYLDACREGSDKPYQLDTNLVNGPLVQENLYGMOVYSWNDNGKP
DQKTIIYLAGGSYLNNPTTYHINMLKTLSTSLDAKIVLPIYPKAPRYTYNYTMPKLVN
LYGHYYHKONGVYELMGDSAGGGALGLAHALHNESVPQPKQLVLLSPWLDVTKSHPEI
DYKEDADPILSSWGLKRVGELMAYSADNTNHIYVSPKNGPITYLPPITLFTGTREIFY
PDIRDYAAKLKAANHITFITQEGNNHVYPIYPIEBKTAQYQIIDAINKTP"
COMPLEMENT (1239. . 1589)
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the complete
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pyogenes MGAS8232]"
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/db_xref="GI:21905238"
/translation="MXHPIRKTLVTLGLLLTLCLPTPAAASSRSWKSWFIEQYFWLKR
                                                                                                                                                                                                                                                                                                                                                                                         6111
                    5290 CCAGAACTATTAGCCCGTCAAGTCATGGAGCCTGTTCGTTTTTATGACAGTGTTGCGACT 6231
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Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
Hamilton, MT 59840, USA
Location/Qualifiers
                                                                                                         840
                                                                                                                                                                                                                                                                                               900
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Phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 50416)
Beres.S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
                                                                                                                                                                                                                                                                                               TITGITAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                    6170 ririgigakgaaarrigaraaarriracrargracragigirgaaaacarggraagcria
                                                                                                         781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
                                                                                                                                                                                          5230 TTAGTAGAAAGTGGCATAACACAATTCATTGAGGTAGGACCAGGTAAGGTTTGACAGGT
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Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)
2. (bases 1 to 50416)
Beres, S.B., Sylva, G.L., Barbian, K.D., Lei, B., Hoff, J.S.,
Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,
Parkins, L.D., McCormick, J.K., Leung, D.Y.M:, Schlievert, P.M.
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Streptococcus pyogenes MGAS315
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae,
Streptococcus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear
section 30 of 37 of
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    .50416
    /organism="Streptococcus
/strain="MGAS315"

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/note="best blastp hit:
esterase [Streptococcus
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AE014165 AE014074
AE014165.1 GI:21905237
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/note="group: A"
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/note="SpyM3_1494"
complement(1239. .1589)
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Direct Submission
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AE014165/c
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AUTHORS
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JOURNAL
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KEYWORDS
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Verptwydydyvytisgdvsbasearrannealeslosidvlynnagitndklakkate
Edpervlkinltgafnmtgoylkpmikarqgaiinvssvvgitgnigqanyaaskagm
IGFTKSVAREVAARIVCVAAIAPGFIESDMTGVLPEKMQEQILSQIPMKRIGKAQEYA
HLASFLVBQDYITGQVIAIDGGMTMQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6950 GATTTTTATGATAACTTTGCTATTGTAAGAAAACCTTTGATCAAGCTAGTCAAGTATTG 6891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5890 GGATACGATTTGCGCCGTTTGATTGATAGTGACGAGTTAAAACTTAATCAAACTAGCTAT 6831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6830 Acecaaccaecratringacarcarcaariscratraccererringescrracarcac 6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6770 GTTAAACCGGATATGGTAGCTGGTCTTTCCTTAGGAGAATACTCAGCTTTGGTAGCATCA 6711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6710 dececacioninida de la controción de la decomposor de controlos de son de controlos de contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6410 deirigriadakenderadengenterrerregenakananganangangan 6351
D. A., Whitton, M., Regers, J. and R. A. VanBogelen. 2000. Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins. Unpublished data.; Best Basetp hit = dbj|BAR06210.1| (AP001515)
3-oxoacyl-(acyl-carrier protein) reductase [Bacilus halodurans]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGCAAGAAGCAGGIGCCAAACGCIIGAIICCICTIAAGGIGICAGGICCCIIICACACC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTICIATGATCAGIATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TATCAGCCTGATATGGTTGCTGGTTTGTCTTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCAGCTCTTGACGCGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGACTAAAACAGCCTTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6530 Acticitacticalariticitadiridericalecacacidiciticalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalectericalec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 439.4; DB 1; Length Pred. No. 1.8e-109; 0; Mismatches 301; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.7%;
ilarity 67.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
620; Conserv
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Best Local S
Matches 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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GOMDTHEMENT (6615. .7151)
complement (6615. .7151)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SpyM3_1502"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTTTEQELTLTPLRGKSGKAYKGTYPNGECVFIKLNTTPILPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (8045. .8836)
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complement (8045. .8836)
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transcription termination-antitermination factor
[Streptococcus pyogenes MI GAS]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transT_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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complement (4676. .4978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4676. .4978)
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/note="SpyM3 1496"
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QQEAKRLAELARQEAKEALKAQAEEMSHREAALKSIEEAETKLKSSNISAKSTADNR
RKKQARPERKNELTHHSQEGÇKCNKKSMNSQNOYRNOKNNNNOKKTKKGKNACNTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="WVEHAKYLGLDVKSHASSVEEADAKKIISSFSKASKPDVTASQT
VKPKEVAQPSVTVVKETGSEHVEKTQVSKPKSRNFKAEREARAKEQAARKQANGSSHR
SQERRGGYRQPNNHQTNEQGDKRITHRSQGDTNDKRIERKASNVSPRHDNHQLVGDRN
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STAMGGECEFVEISAKFNKNIDELLETVLLVAEVEELKADPTVRAIGTVIEARLDKGK
GAIATLLVQQGTLHVQDPIVVGNTFGRVRAMVNDLGRRVKSAEPSTPVSITGLNETPM
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/gene="beyM3 1497"
/note="best non-648 blastp hit: gb|AAK74710.1| (AE007365)
conserved hypothetical protein [Streptococcus pneumoniae
TIGR41, and gb|AAK99283.1| (AE008427) Conserved
hypothetical protein [Streptococcus pneumoniae R6]"
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'transI_table=11
'transI_table=11
'producE_aronserved hypothetical protein"
'protein_id="AAM80104.1"
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protein_id="AAAM80102.1"
/db_xref="G1:21905240"
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/gene="SpyM3 1497"
complement (4971. 5267)
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complement(5283. .6428)
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/note="SpyM3_1495"
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                                                       1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
                                                                                      30296 Argacaaagacarcrirrrarringcedgreaagagaraaaarragagaragedaag
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 Pred. No. 1.9e-109;
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Best Local Similarity 67.3%;
Matches 620; Conservative
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BCT 03-APR-2002 of 173 of the

AE010088 14455 bp DNA linear Streptococcus pyogenes strain MGAS8232, section 136 complete genome.

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/product="conserved hypothetical protein"
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GDEHNDTEMLAFAGTGYAMKNASPVLLPYADQQLNFSNEEDGVAKKLEELFL 1 (bases 1 to 14456) Smoot, J.C., Barbian, K.D., Van Gompel, J.J., Smoot, L.M., Chaussee, M.S., Sylva, G.L., Sturdevant, D.E., Ricklefs, S.M., Porcella, S.F., Parkins, L.D., Beres, S.B., Campbell, D.S., Smith, T.M., Zhang, O., Kapur, V., Dally, J.A., Veasy, L.G. and Musser, J.M. Genome sequence and comparative microarray analysis of serotype MI8 group A Streptococcus strains associated with acute rheumatic fever St., /trānslation="WGIGIIIASHGKFAEGIHQSGSMIFGEQEKVQVVTFMFNEGPDD LYCHFNNAIQQFDADDEILVLADLWSGSFNQASRVAGENBDRKWAIITGLNLPMLIQ AYTERLMDAGAGVEQVAANIIKESKDGIKALPEDLNPVEETAATEKVVNALQGAIPAG TYGDGKLKINLARVDTRLHGQVATAWTFASKADRIIVASDEVAQDDLRKQLA PGGYKANVVPISKLIEASKDPRFGANHALILEQTPQDALRAYEGGVEINELNYGSMAH STGKTMVNNVLSMDKEDVATFEKLRDLGVTFDVRKVPNDSKKNLFELIQKANIK" 1269. .2261 - /gene="spyMl8 1810" /gene="spyMl8 1810" /note="best blastp match gb|AAK34482.1| (AE006602) mannose-specific phosphotransferase system component IIAB [Streptococcus pyogenes Ml GAS]" Ή. Ξ /gene="spyM18 1803" /note="best blastp match gb|AAK34481.1| (AE006602) conserved hypothetical protein [Streptococcus pyogenes . GAS]" 4th 11911.05

2 (bases I to 14456)
Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.B., Ricklefe,S.M.,
Chaussee,M.S., Sylva,G.L., Surdevant,D.B., Ricklefe,S.M.,
Porcella, S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.George, and Musser,J.M.
Direct Sibmission
Submitted (31-JAN-2022) Laboratory of Human Bacterial
Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. 4th
Hamilton, MT 59840, USA Streptococcus pyogenes MGAS8232. Streptococcus pyogenes MGAS8232 Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, /product="mannose-specific phosphotransferase Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002) 21927593 /organism="Streptococcus pyogenes MGAS8232" /strain="MGAS8232" /db_rref="taxon:186103" /protein_id="AAL98330.1" /db_xref="G1:19748919" 105. .917 /gene="spyM18_1809" //cone="spyM18_1810" | 1269. .2261 table=11 component IIAB" 'note="phi_SDA" gene

1-

CDS

gene

CDS

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                                                                                                                                                                                                                                                                                                                      /translation="MTDVSRVIKEARDQGRLTTLDYANLIFDDFMELHGDRHFSDDGA
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QKAKETTGLHEAVLTGKAMVKGQQIALAIMDSHFIMASMGTVVGEKITRLFELAIEEN
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MEGDIILAEPQSLVGFAGRRVIETTVRENLPDDFQKAEFLQDHGFVDAIVKRTELRDK
IAHLVAFHGGGQ"
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putative acetyl-CoA carboxylase biotin carboxylase subunit
[Streptococcus pyogenes M1 GAS]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
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                                                                                                                                                                                                                transl_table=11
/produce== putative acetyl-CoA carboxylase alpha subunit"
protein id="MAL98335.1"
/db_xref="GI:19748924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="putative acetyl-CoA carboxylase beta subunit"
protein id="AAL98336.1"
'db xref="GI:19748925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13330 ATGACAAAACAGCTTTTTTTTTTGCCGGTCAAGGTGCCCAAAATTAGGGATGGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13150 ACGCAACCAGCTATTTTGACATCAATTGCTATTTACCGTGTTTTGGGCTTACATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="accb"
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putative acetyl-CoA carboxylase beta subunit
[Streptococcus pyogenes M1 GAS]"
                                                              /gene="accA"
/note="best blastp match gb|AAK34487.1| (AE006603)
purative acetyl-CoA carboxylase alpha subunit
[Streptococcus pyogenes MI GAS]"
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Pred. No. 4.9e-109;
0; Mismatches 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="accD"
/note="spyM18_1816"
complement(7229. .8095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8104. .9468)
/gene="accC"
/note="spyM18_1817"
complement (8104. .9468)
         /note="spyM18_1815"
complement(6462. .7232)
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trans1 table=
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67.2%;
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Matches 619; Conserv
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ALAAISQLTLIAMGVIGVAIAFIYLNLSKKGGNGGNAAGSADPIGDILEDY"
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ELADTNFVLIPTAEVPLINYYRGEILDGKELPIYFTAMSPSFRSEAGSAGRDTRGLIR
LHQFHKVBMVKRAKPERSPESSYQELKOMTANBNILDKLGLBYRVISLCTGDMGFSAAKTY
DLEVWIPAQNTYREISSCSMTEDFQARRAQIRYDEADGKVKLLHTLNGSGLAVGRTV
AAILENYQNEDGSVTIPEVLRPYMGGETVISPK"
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GWMGPLAGIGDPVFWFTVRPILGALGASLASTGNIVGPLLFFFGWNLIRMAFLWYTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGYKAGSEITKDMSGGILQDITKGASILGMFILAVLVORWVSINFTIDLPGKQLSDGA
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LKKKVSPIAIIIGLFAFGILAHLAGIM"
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ITLPTLMQTFINKFFRH"
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VLEMVEHDSVPVABADEDNVBIRKMOTPRDPDFSVKAHWDLGBDLDLLDWEKGAKVTG
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/gene="spyM18 1813"
/note="best blastp match gb|AAK34485.1| (AE006602)
conserved hypothetical protein [Streptococcus pyogenes M1
GAS]
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putative seryl-tRNA synthetase (Streptococcus pyogenes M1
                                                                                                                                                                                                   /product="putative mannose-specific phosphotransferase system component II" /protein_id="AAL98331.1"
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2350. 3159 "

gane="spyM18 1811"
/noce="bastp match gb|AAK34483.1| (AE006602)
putative mannose-specific phosphotransferase system
component IIC [Streptococcus pyogenes M1 GAS]"
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putative mannose-specific phosphotransferase system
component IID [Streptococcus pyogenes M1 GAS]"
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db_xref="GI:19748922"
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/protein id="AAL98334.1"
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/gene="serS"
/note="spyM18_1814"
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'trans1_table=1
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trans1 table=
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/transl_teable=11
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/note="EVIDENCE BY HOMOLOGY BIO07.01 FATTY ACID AND
PHOSPHOLIPID METABOLISM. General. KEY COMPONENT IN DE NOVO
FATTY ACID BIOSYNTHESIS"
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IGLTKBIARSYAARNYRNNAVAPGFIESDMTEVLSDKVKDAMKGQIPMKRFGMPEEIA
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IPPEBAVKLYAKROYMTSAPAPIGSKYVAVMYIPPBALIESICQKAARFKGIVSPAN
YMTPAQIVIGGEVRSYDXAVELLKRAGVRKLIELKVSGPFHTAILKRASEKLALELD
IDFRPFELPLISNYSAKVMENDEVKGLLIRQVMEPVRFYESVETMQKLGATRFIEUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="malonyl coA-acyl carrier protein transacylase (EC 2.3.1.39)"

fprotein id="hak04871.1"

db xref="GI:L272892"
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/gene="fabG1"
/hote="fabG1"
PHOSPHOLIPIO BETABOLISM. General. FIRST REDUCTION STEP
THE FATTY ACID BIOSYNTHESIS PATHWAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier protein synthase II
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/product="3-oxoacyl-acyl carrier protein reductase
                                                                                                                 organism="Lactococcus lactis subsp. lactis"
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       Jouy en Josas 78352, France
Location/Qualifiers
1. .10701
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2399. .3628
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                                                                                                                                                                                                                                                                                          gene="acpA"
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           Vilvert,
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                                                 FEATURES
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GTTAAACGGGATAIGGTAGCTGGTCTTTCCTTAGGAGAATACTCAGCTTTGGTAGCATCA 13031
                                                                                                                                                                      GGGGCACTCTTTTGAAGATACCCTATCCTTAGTAGTAAGAAGAGCCGCTTGATGGAG 12971
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGAAGAAGATCTGTCAAATAGCTGCTAAACATGGAGTGGTTGCTCCAGCAAACTATAAT 12851
                                                                                                                                                                                                                                                                                                                         GAAGCAGCACCACAAAGATCTGGAAAGATGGTTGCCGTTATGAATACAGACGTGCAAGTC 12911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Traaaggaaagggagrraagggrriraarcccrrraaaggrgricaggrccrrrccacacr 12731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTTGTTAGAACCAGCTAGCCGCTTGTTGGCTAAAGAGTTGGAAAGATACAACTTCAGT 12671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTGAAGAAAATTGATAAAAATTTACTATGTACTAGTGTTGAAAACATGGTAAGCTTA 12431
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                                                                                                             GCCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA
                                                                                                                                                                                                                                                         GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                             421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 ACACCTGCACAAATCGTCGTTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA
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Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
Submission
Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 10701)
Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis 111403
Genome Res. 11 (5), 731-753 (2001)
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Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
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Lactococcus lactis subsp. lactis IL1403
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AE006311 AE005176
AE006311.1 GI:12723690
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                                                                                                                                                                                                                                                                                                                                                                                          /note="EVIDENCE BY HOMOLOGY BIO07.01 FATTY ACID AND PHOSPHOLIPID METABOLISM. General. FIRST STEP IN LONG-CHAIN FATTY ACID SYNTHESIS"
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subunit alpha (EC 6.4.1.2)"
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Pred. No. 1.4e-95;
0; Mismatches 322;
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Best Local Similarity 64.6%;
Matches 598; Conservative
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                                                  TGISVAAEVKEFPEDKYFQKKDARRMDTFSLYAVYAALDAMEMSGITEENTNFDRLGC
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Vibrio cholerae.

Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

(bases 1 to 14530)

Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,

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Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,

Nierman, W.C. and White, O.

DNA, sequence of both chromosomes of the cholera pathogen Vibrio
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1335 GAAGTCAAAGGACTTTTGACGCGTCAAGTCATGGAACCAGTTCGTTTTTATGAATCGGTT 1394
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                                                                                                                                                                                                                       1275 TTTAGACCTTTTGAATTACCATTAATCTCAAATACGAGTGCTAAAGTAATGGAAAATGAT 1334
                                                                                                                                                                                                                                                                                                                                                                                                                 1395 GAAACAATGCAAAACTAGGGGGACTCGCTTTATTGAAGTTGGTCCTGGGAGAGTACTT 1454
                                                                         654
                                                                                                                                                                                                                                                                                                                                                                     775 GGGGTCATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTG 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   835 TCAGGITTIGITAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCG 894
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                                                                                                                                                                     655 TITICAGATITITACTIGICCCCTAGICGGCAATACAGAAGCTGCTGTGATGCAAAAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGCGATTGCTAAAGCCTGTGCTGACGCGGCGCAAGGTGAAGTGGTTTCTCCTGTAAAC 11158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGCGCGTTGATGAAGCCTGCTGCCGGATGAATTGGCAAAAACTCTAGCAGAGCTTGAA 10978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10857 GITGAACAAATGAGCGCACAAGGTGTCGAAAAGCTGATTGAAATGGGGCCGGGTAAAGTA 10798
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VEQLGVDEAEVKNESSFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTVQAAI
DYVTSNAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGCGCCCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAGTAAGTTTGCTATCGTATTTCCAGGTCAGGGCTCGCAAGCAGTAGGTATGCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCTTGCCGAGCAGTATGCTGGTAAAACAAACATTCGCCGAAGCTTCAGAAGTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTATGATTTACGTTATCTCATC - - GATACGGAAGAAGAACAAACTCAATCAGACCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCCAAGGTGCCCAGTATCTAGGGATGGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11517 GGTTACGATCTGTGGGGGCTTCAAGATGGCCCTGTGGAAGATCTCAACTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG---CTATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACTITIGCAAGAAGCAGGIGCCAAACGCITIGAIICCITCIIAAGGIGTCAGGICCCITI
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 219.6; DB 1
Pred. No. 3.9e-49;
); Mismatches 414
                                                                                                                                                                                                                                                                       /gene="VC2021"
complement(9952..10698)
/gene="VC2021"
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          table=11
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larity 54.5%;
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SQAYQGGGRQIAPSTMQSLKQTALGDFKPDLTLYLDIDPKLGLERARGRGELDRIEKM
DISFFERARERYLELANSDDSVVMIDAAQSIEQVTADIRRALQDWLSQVNRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MIKKRVLVLVALIGIVAGSYFYVVKQMDQYLAQPIMIQEAQLVT
IASGTTLSRELAQLTEQAMIQDSFVAEWVRRFHPELSKIKAGTYKLQPDMSLEQALAL
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                                                                                                                                                                                                                                                                                                'translation="MNAKFIVIEGLEGAGKSTAIQVVVETLQQNGIDHITRTREPGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MSRFFLWSESMYWVNGQRRNEVPIHDRSFQYGDGCFTTILTKEG
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AQQQEIPIVIDEFTLEDLLSAEEVFITNALLEVAFVTQIGQQRLTIGSMTRRPGESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="3-oxoacyl-(acyl-carrier-protein) synthase II"
/protein id="AAP95167.1"
/brotein id="AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAIGSGIGGLELIETGÄQALIEKGPRKVSPFFVPSTIVNMIAGNLSIMRGLRGPNIAI
STACTTGLHNIGHAARMIAYGDADAMVAGGAEKASTPLGMAGFGAAKALSTRNDEPQK
ASRPWDKDRDGFVLGDGAGIMVLEEYEHAKARGAKIYAEVVGFGMSGDAYHMTSPSED
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STKSMTGHLLGAAGSVEAIITVMSLVDQMVPPTINLDNPEEGLGVDLVPHVARKVESM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="similar to PID:1173841 PID:1173844; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VC2019"
/note="similar to PID:1173841 SP:P55338 PID:1173843;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VC2020".
hote="aimilar to PID:1173841 SP:P55337 PID:1173842;
dentrified by sequence similarity; putative"
/codon_start=1
                               /note="similar to GB:L42023 SP:P44719 PID:1003796
PID:1222388 PID:1204706; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="4-amino-4-deoxychorismate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _note="identified by Glimmer2; putative"
(codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence similarity; putative"
                                                                                                                                                              /transT_table=11
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/db_xref="GI;9565560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (6253. .7269)
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'transī_table=
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/trānslation="MLTYLEQKINYEFKDKTLLLEALTHSSWAHEGKNEKVSNERLEF
LGDSVLSIVISEYLYKNRKDLEEGSLSKYRAEIVCEPSLARCARKIELGSFLRMGKGE
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       EVI EKEGI KGKKI SI FCNERKLSTVI GQKKYNKR FLEDKYGLQVQVKLLEKI EEDKI V
LSYDKKLYPI SI TDFI KDNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="3-oxoacyl-(acyl-carrier-protein) synthase"
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PFDLNRDGFVMGEGSATL I LESLEHAQKRGAK I YAEI I GYGATDDAYH I TAPAPEGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AARAWBAALKOGKYGYDWUYINAHGTSTBYNDKFETWAIKKYFKDHAYKLCYSSNKS
MLGHLLGAAGAVEAVATVLTITHGIVPPTINYQTPDPECDLNYVPNKAIEREVNYAIS
NSFGFGGHNATLLFKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry Ribonuclease_3, RNase3 domain., score 139, E-value 6.40E-38" complement(1833. .1837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry ketoacyl-synt_C, Beta-ketoacyl
synthase, C-terminal domain, score 238.8, E-value
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AP00155) ribonuclease III [Bacillus halodurans], score
193, E-value 1.00E-48"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Fabb"
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3-oxoacyl-[acyl-carrier-protein] synthase (EC 2 3.1.41)
Bacillus subtilis gi|2633471|emb|CAB12975.1| (299109)
Similar to 3-oxoacyl- acyl-carrier protein synthase
[Bacillus subtilis] gi|2633488|emb|CAB12991.1| (Z99110)
Similar to 3-oxoacyl- acyl-carrier protein synthase
[Bacillus subtilis] gi|2633489|emb|CAB12991.1| (Z99110)
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7.70E-85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry dsrm, Double-stranded RNA binding motif, score 85.2, E-value 1.30E-21" complement(1434. .1706)
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complement(1849..3078)
                                                       complement (1091. .1108)
/gene="ELP3"
/note="putative rho-ind
complement (1137. .1837)
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complement (3111. .3127)
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                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis strain MB4T, section 132 of 244 of the complete genome.
AED13105 AED08691
AED13105.1 GI:20516482
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THEBLIBLKKHDV9VIELGVQSMEDDVLEKSSRGHTSEDVNAVNIL KRYDFKLGLQ
IMIGLAGDTEEKSIATARK VSKRDPRPRIVENTYLEKOV KEGKYTPLSLEQA
INI SKKWYI I FVKAGI DVIRI GLQTTDNI NFNKDVVAGPFHPANGQLVESSI MLDVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 11845)
Boo'Q. 'Itan,Y.' Li,W.' Xu,Z., Xuan,Z., Hu,S., Dong,W., Yang,J.,
Chen,Y., Xue,Y., Xu,Y., Lai,Y., Huang,L., Dong,X., Ma,Y., Ling,L.,
Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H.
A Complete Sequence of the T. tengcongensis Genome
Genome Res. 12 (5), 689-700 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
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                                                                                                                        10737 GCTTCTTTGGATGCGGTGAAATAACAAGAG 10708
                                                                              921
                                                                           892 GCGAGTTTAGTAGCACTTTTAGAAAATAG
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complement(76. ,1153)
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      GAAATATACGAAAATACGAAGAAGCGAAAGAAATTTTTGAAAGGAGCAGATGAGGCTTTA
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                                                                                                                                                         TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAG
                                                                                                                                                                                              AACACACAGCCGGCCATTTTGACAGTTTCAGTGGCCTTGACAAGGGTTTTGCAGAAAAGA
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                                                                                GGTTATGATTTACGTTATCT---CATCGATACGGAAGAAGACAAACTCAATCAGACCCGC
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                                                                                                                                                                                                                                                                                                             AGCGGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATG
                                                                                                                                                                                                                                                                                                                                                                                       GAAGAGGGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAG
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Bacillus licheniformis
Bacteria, Firmicutes; Bacillales, Bacillaceae, Bacillus.
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Sequence 1143 from Patent WO0229113.
AX432728
AX432728.1 GI:21657532
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/protein id="AAAV36931"

/db_xref="G1:0516486"

/translation="MLTEEWLCNIISVQFLRGGEKGMIFEKVRNIIAEQLGIDPEBI

/translation="MLTEEWLCNIISVQFLRGGEKGMIFEKVRNIIAEQLGIDPEBI

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complement (3151. 3354)
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                                                                                                          /note="Best Blastp hit = gi|3912967|sp|067611|ACP_AQUAE ACYL CARRIER PROTEIN (ACP) gi|7442262|pir||A70448 acyl acrier protein - Aquifex acolicus; acolicus; gi|2984024|gb|AACO7567.1| (AE000752) acyl carrier protein [Aquifex acolicus], score 75.5, E-value 2.00E-13"
                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfām match to entry pp-binding, Phosphopantetheine attachment site, score 95.2, E-value 9.80E-25" complement (3407. .4163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Best Blastp hit = gi|7404378|sp|P71019|FABD BACSU
MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (MCT)
gi|7433733|pir||H69620 [acyl-carrier-protein]
/note="putative rho-independent transcription terminator"
complement(3133, .3432)
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S-malonyltransferase (EC 2.3.1.39) fabb [validated]
Bacillus subtilis gi|2337819|emb|CAA74249.1| (Y13937)
putative Fabb protein [Bacillus subtilis]
gi|2633962|emb|CAB13463.1| (Z99112) malonyl CoA-acyl
carrier protein transacylase (Bacillus subtilis], score
276, E-value 2.00E-73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry adh short C2, Short chain
dehydrogenase/reductase C-terminus, Score 59.2, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGACTAAAACAGCCTTTTTATTTTGCTGGTCAAGGTGCCCCAGTATCTAGGGATGGGACGG
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U59433) 3-ketoacyl-acyl carrier protein reductase
Bacillus subtilis], score 265, E-value 6.00E-70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry adh_short, short chain dehydrogenase, score 283.1, E-value 3.60E-81"
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Pred. No. 3.7e-47;
0; Mismatches 421;
                                                                     complement (3133. 3432)
/gene="AcpP"
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Berka, R. and Clausen, I.G.

AUTHORS

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Methods for monitoring multiple gene expression Patent: WO 022913.4 1143.11-APR-2002; Novozymes Biotech, Inc. (103); Novozymes A/S (DK) Location/Qualifiers
                                                                                            1. 950
/organism="Bacillus licheniformis"
/db_xref="taxon:1402"
_223 c 259 g 192 t
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Search completed: June 11, 2003, 18:44:52 Job time : 2441 secs Streptococcus poly N-terminal coding Enterococcus faeca Enterococcus faeca

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FabD protein; malonyl-CoA:ACP family; diagnosis; infection; vaccine;
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AAS52391
ABQ70706
AAV37406
ABN68641
AAX30880
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AAA81489
ABN92524
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ID AAV3
 DNA encoding a Fab
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Streptococcus pneu
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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The present invention relates to nucleic acids (AAH90701-AAH90918)
encoding polypeptides (AAM01002-AAM01114), which are essential for the
viability of a bacterial cell wall. The acronym CFE stands for "CEG For
Expression", where CEG stands for "Conserved Essential Gene". The nucleic
acids are useful for detecting the presence of proteins essential for the
viability of a bacterial cell wall in samples such as cells, tissues,
biological fluids, blood, serum, nose, ear or throat swabs with ligands,
and for detecting corresponding target nucleic acid molecules with
complementary sequences. The nucleic acids are also useful for
determining whether a genomic nucleotide sequence of interest is
cesential for viability of a bacterial cell or whether it resides within
an operon, by integrating an exogeneous nucleotide sequence of interest
comprising 200-500 base pairs) into the genomic sequence of interest
which confers a selection agent such as chloramphenicol. The nucleic
comprising the selection agent such as chloramphenicol. The nucleic
cids and proteins are also useful as vaccines and for treatining bacterial
infections with gene therapy and antisense therapy. The nucleic acids
also enable identification of targets suitable for the treatment of
TITIGITAAAAAATIGATCAAACIGCICACITAGCICAIGIGGAAGAICAAGCGAGITTA
                                                                                                                                                                                                                TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding conserved essential genes involved in tion which are potential targets for the treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication which are potential resistant bacterial infections
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                                                                                                                                                                                                   The present sequence encodes a FabD protein of Streptococcus pneumoniae 0100993 (NGTMB 40800). The novel FabD polypeptides are related to other proteins of the malonyl-COA.RCP family. The products can be used for the diagnosis of Streptococcus pneumoniae infections. Vectors containing the FabD DNA sequence can be administered directly to a mammal to produce the FabD poptide to provoke an antibody/T-cell response in order to prevent a disease. The peptide can be used to screen for compounds which modulate its activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                New isolated Streptococcus pneumoniae FabD gene - used to develop products for the diagnosis, prevention and treatment of bacterial diseases, particularly S. pneumoniae infection
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Pred. No. 3.1e-281;
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Best Local Similarity 100.0%; Pred. No. 3.1
Matches 921; Conservative 0; Mismatches
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WPI; 1998-312173/27.
P-PSDB; AAW60856.
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                                                                                   Gaps
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                                                       Length 921;
                                                                                Indels
                           Sequence 921 BP; 246 A; 193 C; 232 G; 250 T; 0 other;
                                                                                 'n
                                                   Score 913; DB 22;
Pred. No. 1.1e-278;
0; Mismatches 5;
 antibiotic resistant bacterial infections.
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                                                    Match 99.1%;
Local Similarity 99.5%;
Les 916; Conservative
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the rucleic acid molecule sproduced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the Indiany which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleic degenere is homologues to amplification primer derived from the fragment of the S. pneumoniae genome to prime the mamplification and isolating the amplified sequences. The computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           readable medium can be used in a computer-based system for identifyin fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                        S. pneumoniae, genome, diagnosis, ass
vaccine, pharmaceutical composition;
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Local Similarity 99.5%; Pred, No. 5.8e-278;
Les 916; Conservative 0; Mismatches 5; Indels 0;
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                                                                                                                                                    fragment SEQ ID NO:7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dougherty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 194-205; 1409pp; English
                                         BP
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                                                                                                                                                      Streptococcus pneumoniae genome
                                         AAV52140 standard; DNA; 19702
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                                                                                                                                                                                                                                                                                                                                                                                                   96US-0029960.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                 entry)
                                                                                                                                                                                          Streptococcus pneumoniae;
computer readable medium;
                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-272225/24.
                                                                                                                 (first
                                                                                                                                                                                                                                                                                      WO9818931-A2
                                                                                                                                                                                                                                                                                                                                                             30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1996;
                                                                                                                 23-OCT-1998
                                                                                                                                                                                                                                                                                                                         37-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae
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Best Local Si
Matches 916;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes them is use in the discovery of novel antiblocits, the essential genes themselves and the discovery of novel antiblocits, the essential genes themselves and the discovery of novel antiblocits, the essential genes themselves and the discovery of novel and proteins. The proteins and the encoded proteins. The protein also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to antiblocic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds to the expressed proteins. The proteins mucleic acid swhich are required for cell proliferation in a wide vartery of organisms. The present sequence encodes an essential processing cellular proliferation protein.

Oute: The sequence data for this patent did not form part to the printed specification, but was obtained in electronic form that directly from WIPO at the printed specification, but was obtained in electronic form the for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGACAAAACTCAATCAGACCCGCTAT 180
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Pred. No. 3.5e-278;
0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                          Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Seq ID No 9482; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                        Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                               23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-25595E.
22-DEC-2000; 2000US-255931P.
16-FEB-2001; 2001US-269308P.
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99.3%;
                                                                                      21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
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Xu HH;
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P-PSDB; AAU37986.
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Matches 915; Conserv
WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto RT,
                                                                                                                              21-MAR-2000;
23-MAY-2000;
                                           27-SEP-2001
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                                                                                                                                                                               This sequence is a gene fragment from the Streptococcus pneumoniae genome. The invention provides DNA sequences (AAV65201 to AAV65304) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAW80605 to AAW80728). A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or apptide fragments can be used to treat S. pneumoniae infection. The antibodies can also be used to detect S. pneumoniae cells.
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                                                                      c acid sequences - used in DNA chips and identification of virulence
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Pred. No. 7.3e-278;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3580 BP; 1035 A; 666 C; 894 G; 985 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae protein, recombinant, gene expression, DNA chip, virulence, antibody, infection, detection, treatment,
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Peery RB, Rockey PK, Rosteck PR;
Solenberg PJ, Treadway PJ;
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                                                                      GAAGCGGCTCCTGCTGA
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Mills BJ, Norris FH, I
Skatrud PL, Smith MC,
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encoding polypeptides (AAM01002-AAM01114), which are essential for the
viability of a bacterial cell wall. The acronym CPE stands for "EGF For
Expression", where CPG stands for "Conserved Essential Gene". The mucleic
acids are useful for detecting the presence of proteins essential for the
viability of a bacterial cell wall in samples such as cells, tissues,
biological fluids, blood, serum, nose, ear or throat swabs with higands,
and for detecting corresponding target nucleic acid molecules with
complementary sequences. The nucleic acids sera also useful for
complementary sequences. The nucleic acids sequence of interest is
essential for viability of a bacterial cell or whether it resides within
an operon, by integrating an exogeneous nucleotide sequence comprising a
portion of an open reading frame of the genomic sequence of interest
(comprising 200-500 base pairs) into the genomic sequence of interest
which confers a selectable phenotype to the cell, and determining cell
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                                  GATITIACITGICCCIAGICGGCAAIACAGAAGCTGCTGTGAIGCAAAAAAGGCCAIT
                                                                                                                  TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA
GATITIACTIGICCCCTAGICGGCAATACAGAAGCTGCTGIGAIGCAAAAAGAGGACAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance; ds.
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viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of targets suitable for the treatment of antibiotic resistant bacterial infections.
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                                                                                                                                                           Query Match 98.6%; Score 908.4; DB 2
Best Local Similarity 99.3%; Pred. No. 3.1e-277
Matches 912; Conservative 0; Mismatches 6
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                                                                                                                    301 TCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGACATTGCTCAGCTCTT
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                                                                              TCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATTGCTCAGCTCTT
       This sequence encodes a Streptococcus pneumoniae protein that (based homology with a Cupiea lancedlata protein) is a 3-oxoacyl reductase precursor protein, and represents a DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae protein; genetic immunisation; antagonist; immuniological response; incollation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the C-terminal coding region of Fabb embodiment (coding begins at nucloctide 2) of Streptococcus pneumoniae 0100993 (NCIMB 40800). The novel Fabb polypeptides are related to other proteins of the malonyl-CoB.ACP family. The products can be used for the diagnosis of Streptococcus pneumoniae infections. Vectors containing the Fabb DNA sequence can be administered directly to a mammal to produce the Fabb peptide to provoke an antibody/T-cell response in compounds which modulate its activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Streptococcus pneumoniae FabD gene - used to develop products for the diagnosis, prevention and treatment of bacterial diseases, particularly S. pneumoniae infection
                                                                                                                                                                                                                                                                                      C-terminal coding region encoding a FabD polypeptide embodiment
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ive 0; Mismatches 11
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(SMIK ) SMITHKLINE BEECHAM CORP
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          invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can also be used to induce an immunological response in a mammal by incoulation with the S. pneumoniae proteins or delivery of the encoding mucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein—mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the
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 0100993 (NCIMB 40794). The Streptococcus pneumoniae
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SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.

(SMIK)

96US-0025788. 96US-0014690. 97WO-US05306

01-APR-1997; 22-AUG-1996; 02-APR-1996; Nucleic acids encoding pneumococcal polypeptide(s) vaccines, drug screening, etc

Page 105-106; 354pp; English.

Claim 5;

Nucleic

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AAX30724 to AAX30946 represent genomic DNA sequences isolated from Streptococcus pneumoniae strain 0100993. These genomic DNA sequences encode the novel proteins given in AAY11114 to AAY1137. The proteins, isolated from Streptococcus pneumoniae, can be used in vaccines against streptococcal infections and in assays for identifying compounds that inhibit or activate the activity of the proteins. The antagonists can be used to treat an individual having need to inhibit a bacterial protein. Vectors expressing the proteins can be used to induce a protective immune response in mammals.
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Pred. No. 4.6e-155;
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                  Score 523.2; DB 19;
Pred. No. 4.6e-155;
0; Mismatches 3;
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                                                                     719 AAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCACTT 660
               CAGGCATAAGCAACTTTATTCGAGATTGGACCGGGGAAAGTCTTGTCAGGTTTTGTTAAA 720
                                               850 AAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCACTT

    useful,
    prevention

                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tāg= a
/product= putative malonyl coenzyme A-acyl carrier
protein transacylase homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a coding region isolated from
S. pneumoniae. Its encoded protein, or agonists of it,
c may be useful as an antibacterial for treatment or
prevention of infection, specifically caused by S. pneumoniae
(particularly meningitis) but possibly also Helicobacter
C pylori (ulcers and gastric cancer). It may be of particular
use before insertion of an in-dwelling device or any other
invasive procedure. The protein, or nucleic acid encoding
c it, can also be used in vaccines to induce a callular
and/or humoral immune response, or to screen for other
antibacterials. The DNA may also contain flanking sequences
that are potential sources of control elements for bacterial
gene expression. Detecting a sequence encoding the protein
can be used diagnostically, e.g. to detect a mutation for
serotyping or classifying infectious agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acids from Streptococcus pneumoniae e.g. for identifying anti-bacterial(s) for treatment and of meningitis
                                                                                                                                                                                                                                                                                                                                                      frame; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 336 A; 288 C; 227 G; 358 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knowles DJC, Lonetto MA,
                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
complement (731..1123)
                                                                                                                                                                                                                                                                                                                                                     ion; ORF; open reading frame prevention; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 111-112; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                            ВD.
                                                                                                                                                                                                                       AAV37406 standard; DNA; 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0029930.
                                                                                                                                                                                                                                                                                         entry)
                                                                                                            TTAGAAAAATAG 921
                                                                                                                                         TTAGAAAATAG 648
                                                                                                                                                                                                                                                                                                                                                      region; ORF; open
                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson JE,
Zarfos PN;
                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-286586/25.
P-PSDB; AAW61018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-1997;
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                                                                                                                                                                                                                                                                                       13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                      coding regi
infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black MT,
                  779
                                                                                                              910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reid RH,
                                                                                                                                           629
                                                                                                                                                                                                                                                         AAV37406
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                                                   rrrigrgaagaaarrigaraaaarrracrargracragrgrrgaaaacarggraagcrra
                                                                                                                   GCTCTCCTTGAGCCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA
                                                                                                                                                                                                                                                      GACTICAAGATICCTTIGGITGGTAATACCGAAGCTAATATTATGGAAAAAGACCGTATC
                                                                                                                                                                                                                                                                                                                                        CCAGAGACTATTAGCCCGTCAAGTCATGGAGCCTGTTCGTTTTTATGACAGTGTTGCGACT
                                                                                                                                                                                                                                                                                                                                                                                              781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tragradadagocaraacacaarrcarrdagoragoaccagoraagorrrrgacagor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITGITAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA
                        TIGCAAGAAGCAGGIGCCAAACGCIIGAIIICCICIIAAAGGIGICAGGICCCIIIICACACC
                                                                                                                                                             GCTTTGTTAGAACCAGCTAGCCGCTTGTTGGCTAAAGAGTTGGAAAGATACAACTTCAGT
                                                                                                                                                                                                          GATITIACTIGICCCCTAGICGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGACAIT
                                                                                                                                                                                                                                                                                                     - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genomic DNA sequence SEQ ID NO:157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae strain 0100993; vaccine; immune infection; pneumococcal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding pneumococcal polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGITITATITIAGATAGAGAG 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 150; 354pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGCACTTTTAGAAAAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines, drug screening, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0025788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0014690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX30880 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US05306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-503111/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY11297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9737026-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black MT,
                                                                     547
                                                                                                                   601
                                                                                                                                                             607
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AAX30880

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AAX30880

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AAX30

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                                                                                                                                                                                                                                                                                                                                     The interior relates to a protein (ABE/29413-ABF10803) from group A streptococcus (GRE (Greptococcus agalactice) or group A streptococcus (GRE).

(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibocterial and antibiflammatory activity. (I), nucleic acids encoding (I), ABN60044-ABN71526 and antibocises that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by CS Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be cheed in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATTTTTATGATAACTTTGCTATTGTAAGAAAACCTTTGATCAAGCTAGTCAAGTATTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGCACTCTTTTGAAGATACCCTATCCTTAGTAGCTAAGAGGCCGCTTGATGGAG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGACAAAGACAGCCTTTTTTATTTGCCGGTCAAGGTGCTCAAAAATTAGGGATGCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGATACGATTTGCCCCTTTGATTGATAGTGACGAGTTAAAACTTAATCAAACTAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTTATTGCAAGAAAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCAACCAGCTATTTTGACATCATCATTGCTATTTACCGTGTTTTGGGCTTACATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 GTTAAACCGGATATGGTAGCTGGTCTTTCCTTAGGAGAATACTCAGCTTTGGTAGCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGCACCACACAAGCATCTGGAAAGATGGTTGCCGTTATGAATACAGACGTGCAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
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                                                                                                                                                                                                                                                                                                                         invention relates to a protein (ABP25413-ABP30895) from group B
                                                 Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                 Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 942 BP; 285 A; 159 C; 217 G; 281 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 439.4; DB 24;
Pred. No. 1.5e-128;
0; Mismatches 301;
                                              Margarit Ros YI,
                                                                                                                                                                                                                                                                            Claim 7; Page 3863; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%;
ilarity 67.3%;
Conservative
                                            Masignani V,
(GENO-) INST GENOMIC RES
                                                                                                                 WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 620; Conserv
                                                                                                                                       P-PSDB; ABP28010
                                         Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB5521). The nucleic acid sequence; is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Date this patent is based on equivalent patent WO200177334 (published 18-07-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                     782872 ATGACTAAAACAGCATTTTTATTCTCAGGTCAAAGGGGCACAAAAGCTTGGAATGGCACGT
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                                                                                                                                                                                                               Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
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Pred. No. 1.2e-110;
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     or activate the activity of the proteins. The antagonists to treat an individual having need to inhibit a bacterial Vectors expressing the proteins can be used to induce a
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                                                                                                                           Score 402; DB 18; Length 6
Pred. No. 8.6e-117;
Nismatches 5; Indels
                                                                                           Sequence 636 BP; 168 A; 144 C; 156 G; 168 T; 0 other;
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ilarity 98.8%;
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                                    783712 TCAGGITICATTAAAAATIGATAAAATGCAGAAATIGCTAATGTIGAAATITAGCT 783771
             894
                                                                                                                                                                                                                                                                              Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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Score 387; DB 24; Length 924; Pred. No. 6e-112;

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Query Match Best Local Similarity

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                                                                                                             Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, gene, antiinflammatory, infection, vaccine, meningitis, gene therapy, ds.
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42.0%; Score 387; DB 24; Length 2:
Best Local Similarity 64.5%; Pred. No. 4.3e-110;
Matches 595; Conservative 0; Mismatches 325; Indels
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                                                        Streptococcus polymucleotide SEQ ID NO 10967.
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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(first entry)
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(GENO-) INST GENOMIC RES.
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331187 GAACTTAGACCAGATATGGTTGCAGGACTTTCTTTGGGAGAATACAGTGCTTTAGTTGCT 331246
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                                                                              298 AGCGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCCTAAAGCGTGGAGCCTATATG
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e : 275 secs
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Sequence 7, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INFORMENCE: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17149 ATGACTAAAACAGCCTTTTTTATTTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 17090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Pred. No. 8.1e-295;
0; Mismatches 5;
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US-07-757-022B-41
US-07-757-022B-141
US-07-757-022B-49
                                                                    US-08-804-227C-13
US-08-804-227C-7
US-08-804-198-1
US-09-105-537-3
US-09-105-537-5
US-09-320-878-19
US-07-757-0228-13
US-07-757-0228-83
                                                                                                                                                                                                                                                                                                -07-757-022B-57
-07-757-022B-103
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99.5%;
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Best Local Similarity 99.5
Matches 916; Conservative
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TOPOLOGY:
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                                                                                                                                                                      June 11, 2003, 17:59:32 ; Search time 70 Seconds (without alignments) 4034.990 Million cell updates/sec
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Sequence 19,
Sequence 1,
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Sequence 9,
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Sequence 1
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1 atgactaaaacagcctttt......tagcactttagaaaatag
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-8188-207A-8

US-09-134-001C-1987

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US-09-108-517-1

US-09-108-517-1

US-09-090-793-12

US-08-375-709-10

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US-09-370-700-1
US-09-154-083-9
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US-09-078-166-1
US-08-292-467-1
US-08-961-527-7
US-09-105-537-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 523.2; DB 4;
Pred. No. 4.9e-165;
0; Mismatches 3;
                            Beecham Corporation
Road
               ADDRESSEE: SmithKiline Beecham Corporation STREET: 709 Swedsland Road CITY: King of Prussia STARE: PA COUNTRY: USA ZIP: 19406-0939 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DATA: 105 CURRENT APPLICATION DATA: 105 CURRENT APPLICATION DATA: APPLICATION NUMBER: 05/01760 FILING DATE: 14-MAY-1997 STILING DATE: 14-MAY-1996 ATTORNEY/AGENT INFORMATION: NAME: Gimmi, Edward R REFERENCE/DOCKET NUMBER: P50475 TELEFONMUNICATION INFORMATION: TELEFONMUNICATION INFORMATION: TELEFONMUNICATION INFORMATION: TELEFONMUNICATION INFORMATION: TELEFONMUNICATION INFORMATION: TELEFONMUNICATION TELEFONMUNICATION OF 
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Best Local Similarity 99.1%;
Matches 547; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1196 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS
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TOPOLOGY:
US-08-858-207A-8
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                                              .6849 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 16790
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   121 GGTTAFGATTTACGTTATCTCATCGATACGGAAGAAGAAGAAACTCAATCAGACCCGCTAT
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Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Stodolas, Richard
APPLICANT: Stodolas, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
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Sequence 1987, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-07

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779
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481 AAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCACTT 540
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                                                                                                                                                                                       Sequence 1003, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF NUMBER OF SECTIONS: 1120
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alco
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Pred. No. 2e-44;
0; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURREATING SYGTEM: Windows SOFTWARE: FASTERO for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
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APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
FILING DATE: 00-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PC7AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY APPLICATION NUMBER: PC7AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY APPLICATION: NUMBER: PC7AU98/01023
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9686 base pair
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Best Local Similarity 52.8
Matches 452; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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EDNESS: double
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TOPOLOGY: circ
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US-09-221-017B-1003
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                             Length 936;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                             Score 130.4; DB 4;
Pred. No. 1.5e-33;
0; Mismatches 421;
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                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1987
                                                                                                                                                                                                                                                                                                 14.2%;
50.1%;
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1987
LENGTH: 936
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.1
Matches 438; Conservative
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61 GATITCIATGATCAGIATCCGATIGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GACTTIGATATTTTAGAGACAATGTTTACTGATGAAGAAGGTAAATTGGGTGAAACTGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 126.4; DB 1;
Pred. No. 3.2e-32;
0; Mismatches 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOSSION OPERATING SYSTEM: DOSSION OF WINDOWS Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/789,609A FILING DATE: 24-JAN-1997
                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                       No. 5827689el FabD
Sequence 1, Application US/08789609A, Patent No. 5827689, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030685
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                         APPLICANT: Gentry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Pearson, Stewart
APPLICANT: Payne, David
TITLE OF INVENTION: NO. 58276.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 38,891
REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.1%;
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                ZLF: 1330 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 610-270-4478
610-270-5090
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SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gimmi, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                 RY: USA
19406-0939
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61 GATTTGTTTAATAACAATGATCAAGCAACTGAAATTTTAACTTCAGCAGCAAAAGACGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 456;
                                                                                                                                                                                                                                                                                                                                                                                                Score 126.4; DB 4
Pred. No. 3.2e-32;
0; Mismatches 456
                                            38,891
FR: GM50004
  ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: GMS/
TELECOMMUNICATION:
TELECHONE: 610-270-4478
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0
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49.1%;
                                                                                                                                  TELEFAX: 610-270-5090
TELEX: INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                            STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 455; Conserv
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                                            GAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAG
                                                                                                                                     418 GTCATTGAAGAAGCCTGTCA---AAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAAC
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSISEE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,517
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/789,609
FILING DATE:
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Road
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Patent No. 6258934
GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
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APPLICANT: Lonsdale, John
APPLICANT: Pearson, Stewart
APPLICANT: Payne, David
TITLE OF INVENTION: No. 625893
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SAITHKINE Beeche
STREET: 709 Swedeland Road
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Best Local Similarity 46.8<sup>1</sup>
Matches 332; Conservative
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CRGANISM: Vibrio marinus
US-09-090-793-12
                             AAGCTGCTGTG-
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ATTGGGGTCATGCAAGAAGCAGGCATAAGCAAACTTTATCGAGATTGGACCGGGGAAAGTC
                                                     775 ACAGAATGGCTAATAGACCAAGGTGTTGATCATTTTATTGAAATTGGTCCTGGAAAAGTT
                                                                                                             TTGTCAGGTTTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAA
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09090793

Patent No. 6140486
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Production of polyunsaturated fatty acid
TITLE OF INVENTION: of polyketide-like synthesis genes in pl
FILE REPERENCE: CGNE.131.01US
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER PELING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
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Pred. No. 3.1e-12;
0; Mismatches 363;
                                                                                                                                                                                                                 892 GCGAGTTTAGTAGCACTTTTAGAAAA 917
                                                                                                                                                                                                                                                                         GAAGATGTGAAAGGATGGAATGAAAA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.5%;
Best Local Similarity 46.8%;
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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CRGANISM: Vibrio marinus
US-09-090-793-13
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RESULT 8
US-09-09-13-12
| Sequence 12, Application US/09090793
| Sequence 12, Incordant | Sequen
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2932 cadectrodrecatrcaaccaaccaardacarraacaaaaaccreaaaaaccreaaaaccacardc 2991
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                                                                                                                            AGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTCATGCAAGAAGCAGGCATAAGCAACT
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Pred. No. 5e-12;
0; Mismatches 363;
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APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAMADA, Akiko
APPLICANT: KAMO, Seishi
APPLICANT: KATO, Seishi
APPLICANT: MARKATION: ACID
APPLICANT: MARKATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2468 ACGCICAAGCGCCATITGCIAAAGCGATTGACGCAGCCAAAITIACTAAAACAAGCCGAG 2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 CIGCIAGCCAGAAACIAGCIGAAACICIAGCICAGGIAAGITITICAGAITITIACITGIC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2111 TTGGTGAGCTAAGTGCACTGTGTGCTGCAGGTGTTATTTCAGCTGATGACTACAAGC
                                                                                                                                                                                                                                                                                              .991 AAGAAGCCATTTTGACCAATACCGCCAATGCCCCAAAGCCGCAATTGGTGCGATTTCAATGG
                                                                                                                                                                                                                                                                                                                                                                        212 CTATCTACCGFTTATTGCAAGAAAGGGCTATCAGCCTGATATGGTTGCTGGTTTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                    2051 Grcaaracearingrinacrecegenegerinaarecegacaregringeregecarager
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 --GACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAAGAAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACACCGCTCTCCTTGAGC
                                                                                                                                                                                                                                     152 AAGAAGACAAACTCAATCAGACCCGCTATACGCAACCAGCCATTCTAGCGACTTCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 GTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAACACACCTGCACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 TCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTGCAAGAAGCAG
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                                                                                                                                                                      Gaps
                                                                                                                                                                      21;
                                                                                                      Length 8268;
                                                                                                   Score 53.4; DB 1; Length E
Pred. No. 3.6e-07;
0; Mismatches 276; Indels
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3000 K Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08752929
Patent No. 5798259
GENERAL INFORMATION:
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                                                                                                      . 5 . 8%;
                                                                                                   Query Match
Best Local Similarity 46.7
Matches 260; Conservative
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LOCATION:
US-08-375-709-10
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COUNTRY:
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   19855 CTAAAGCGGTTGATAGCGCTAAATTTAAAGCGCCAAGCATTCCAGTGTTTGCTAATGGCA 19914
                                                                                                                                      19915 CAGGCTTGGTGCATTCAAGCAAACCGAATGACATTAAGAAAAACCTGAAAAACCACATGC 19974
                                                                      692 AAGCTGCTGTG-----ATGCAAAAAGAGACATTGCTCAGCTCTTGACGCGTCAGGTCA
                                                                                                                                                                                                  746 AGGAACCCGTTCGTTTCTATGAAGTATTGGGGTCATGCAAGAAGCAGGCATAAGCAACT
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APPLICANT: YAZAMA, KAZUNAGA
APPLICANT: YAZAMA, AKINA
APPLICANT: YAMAMA, AKINA
APPLICANT: KATO, Seishi
APPLICANT: KONDO, KAYOSI
TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Biscosapentaenoic Acid
TITLE OF INVENTION: Biscosapentaenoic Acid
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     20035 Tranchartrigerecaanaakargrantaacraaarrigerigaaacarr 20084
                                                                                                                                                                                                                                                                                                                                        806 TTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGTTTTGTTAAAAAATT 855
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 53,258
REFERENCE/POCKET NUMBER: 53,466/150/AAOK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shewanella putrefaciens SCRC-2874 (FERM
BP-1625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08375709
Patent No. 5683898
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 8268 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 672-5300
(202) 672-5399
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LOCATION:
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NAME/KEY:
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CITY: Wa
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15896 AAGAAGCCATTTTGACCAATACCGCCAATGCCCAAAGCGCAATTGGTGCGATTTCAATGG 15955
       2411 GTTACAAA---GCGATTAACCTGCCAGTATCAGGTGCATTCCACACACTGAACTTGTTGGTC 2467
                                                                                                   2468 ACGCTCAAGCGCCATTTGCTAAAGCGATTGACGCAGCCAAATTTACTAAAACAAGCCGAG 2527
                                                     614 CTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCAGATTTTACTTGTC 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
TITLE OF INVENTION: Eiscosapentaenoic Acid
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AAGAAGACAAACTCAATCAGACCCGCTATACGCAACCAGCCATTCTAGCGACTTCGGTTG
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Pred. No. 9.3e-07;
0; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53466/150/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-MAY-1993
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 15-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTATION NUMBER: 23-258
REFERENCE/DOCKET NUMBER: 53466/150/A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08375709
Patent No. 5683898
GENERAL INFORMATION:
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Kazunaga
APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
                                                                                                                                                                                              2528 CACTITACICAAAIGCA 2544
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                              674 CCCTAGTCGGCAATACA 690
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3000 K Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 37895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (202)672-5399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
FILING DATE: 20-JAN-13
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Best Local Similarity
Matches 260; Conserva
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COUNTRY: USA
ZIP: 20007-5109
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2111 TTGGTGAGCTAAGTGCACTGTGTGCTGCAGGTGTTATTTCAGCTGATGACTACTACAAGC 2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2231 CAGATGCAGGAGCAATGTTTGCAATCATAACCAAGAGTGCTGCAGACCTTGAAACCGTTG 2290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AAGAAGACAAACTCAATCAGACCCGCTATACGCAACCAGCCATTCTAGCGACTTCGGTTG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGCCAAACGCTIGATICCTCTTAAGGIGTCAGGTCCCTTTCACACGCTCTCCTTGAGC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1991 AAGAAGCCATTTTGACCAATACCGCCAATGCCCAAAGCGCAATTGGTGCGATTTCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8268;
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                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JAN-1995
FILING DATE: 20-JAN-1995
FILING DATE: 10-JAN-1995
FILING DATE: 14-MAY-1993
FILING DATE: 14-MAY-1993
FILING DATE: 15-MAY-1993
ATORNEY/AGENT INFORMATION:
NAME: WEGNER, HALCH C.
NAME: WEGNER, HALCH C.
REGISTRATION NUMBER: 55,288
REGISTRATION NUMBER: 55,288
REGISTRATION NUMBER: 25,288
RETERENCE/DOCKET NUMBER: 53466/150/AAOK
TELEPPHONE: (202)672-5399
                         US/08/752,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH 8.268 base pairs TYPE: mucleic acid STRANDEDNES: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: DNA (genomic)
                                                20-NOV-1996
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..8268
                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY;
, LOCATION:
US-08-752-929-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 AAGAAGACAAACTCAATCAGACCCGCTATACGCAACCAGCCATTCTAGCGACTTCGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37895,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Shewanella putrefaciens SCRC-2874 ORGANISM: BP-1625)
                                                                                                                                                  53466/150/AAOK
APPLICATION NUMBER: JP 4-14794
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harcld C.
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 53466
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09090793
Patent No. 6140486
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.7%;
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 37895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-09-090-793-1
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Patent No. 5798259
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Kazunaga
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding for Bicosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Brzymes and Process for Production of Biscosapentaenoic
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                            15956 GTCAATACGATTTGTTTACTGCGGCTGGCTTTAATGCCGACATGGTTGCAGGCCATAGCT 16015
                                                                                                                                                                             TIGGIGAGCIAAGIGCACIGIGIGCIGCAGGIGITATITICAGCIGATGACTACAAGC 16075
                                                                                                                                                                                                                                                                                              TGGCTTTTGCTCGTGGTGAGGCTATGGCAACAAAAGCACCGGCTAAAGACGGCGTTGAAG 16135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16196 AAGCCACCATCGCTAAATTTGATGGGGTGAAAGTCGCTAACTATAACGCGCCAACGCAAT 16255
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                                                                                                                      TIGGAGAATACTCTGCCTTGGTGGCAAGCGGCGCCTTGGATTTTGAAGATGCGGTTGCCT 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 GTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAACACACCTGCACAAA
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                                                                                                                                                                                                                                    TGGTAGCTAAGCGTGGAGCCTATATGGAAGAAGCGGCTCCTGCT----
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APPLICATION NUMBER: US/08/752,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
FILING DATE: 10-JAN-1995
PRIOR APPLICATION DATA:
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/752,925
20-NOV-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 30
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at various positions throughout the sequence a, t, c or g
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                                                                                                                                                                                                                                                                               Score 53.2; DB 4; 1
Pred. No. 2.2e-05;
0; Mismatches 173;
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Pred. No. 2.2e-05;
0; Mismatches 173;
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APPLICANT WHITE, Owen R.
APPLICANT HAITE, Owen R.
APPLICANT WHITE, Owen R.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN J.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION WUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEGUINO: LENGTH: 4411529
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
                                                                                                                               ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GATTIACGTIATC-----
                                                                                                                                                                                                                                                                           5.88;
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Best Local Similarity 49.2%;
Matches 182; Conservative (
                                                                                                                                                                                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.2
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATATGGAAG 361
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US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mycobacterium
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US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 CTATCTACCGTTTATTGCAAGAAAAGGGCTATCAGCCTGATATGGTTGCTGGTTTGTCTC
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APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by ITILE OF INVENTION: Of polyketide-like synthesis genes in plants FILE REPERENCE: CGNE. 131.01US
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
BARLIER APPLICATION NUMBER: 60/048,650
BARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                          Length 37895;
                                                                                                                                                                                                                                                                                                                       Score 53.4; DB 3; Length 37
Pred. No. 9.3e-07;
0; Mismatches 276; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FYSER, Claire M. APPLICANT: VENTER, JOHN C. TITLE OF INVENTION: DNA SEQUENCES FOR TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                           TYPE: DNA
, ORGANISM: Shewanella putrefaciens
US-09-090-793-1
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Best Local Similarity 46.7%;
Matches 260; Conservative
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Length 4403765;
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487676 TATGCTGCCTACCCGGTTTTCGCCGAGGCCCTCGATGCTGTGGTGGACGAGTTGACCGG 487735
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                                                                                                                                                                                                                                                                                                                                                              487856 TCGTGGGGGGGGGCGGGTTTGGTGCTGGGTCATTCGGTGGGCGAGTTGGCCGCGGCC 487915
                                        487616 AAGACGCTTTTGTCTTTGCCGGTCACGCTCCCAGTGGCTGGGTATGGGTAGGCAGCTT 487675
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                                                                                                    232 GAAAAGGGCTATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTG 291
                                                                                                                                                                                                              127 GATTTACGTTATC-----TCATCGATACGGAAGAGACAAACTCAATCAG 171
                                                                                                                                                                                                                                                                                                                      172 ACCCGCTATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 GIGGCAAGCGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCC 351
7 AAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGGGATTTC 66
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Search completed: June 11, 2003, 19:47:06 Job time : 88 secs

Sequence 1191, Applisequence 24, Applisequence 24, Applisequence 264, Applisequence 264, Applisequence 264, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 11, Applisequence 29, Applisequence 30, Applisequence 5, App

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US-94-B-5-44-9482

US-94-B-5-44-9482

Sequence 9482, Application US/09915242

Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Obleen, Rari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Arawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Will H Goward
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Drokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,931
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/259,308
FRIOR FILING DATE: 2001-02-16
FRIOR FILIN
9 US-09-712-363-20

10 US-09-815-242-713

10 US-09-815-242-713

10 US-09-815-242-7145

9 US-10-077-584-3

9 US-10-077-584-3

9 US-10-077-684-3

9 US-10-184-644-264

9 US-10-184-644-332

9 US-10-184-644-332

9 US-10-184-644-332

9 US-10-184-644-332

9 US-09-813-818-1

10 US-09-813-818-1

10 US-09-81-289-1

10 US-09-81-289-3

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CRGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(921)
US-09-815-242-9482
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        Sequence 9482, Ap Sequence 6823, Ap Sequence 1143, App Sequence 11086, App Sequence 6028, App Sequence 618, App Sequence 5522, App Sequence 552, App Sequence 7796, App Sequence 13, App1 Sequence 11, App1 Sequence 13, App1 Sequence 11, App1 Sequen
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/BW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/BO6 NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-815-244-6823
US-09-076-27A-577
US-09-974-300-1143
US-09-974-300-1086
US-09-974-200-1086
US-09-974-26-6978
US-09-815-242-6028
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APPLICANT: Onlean, Mail L.
APPLICANT: Mail, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Mail, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yu. H. Howard
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,931
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-10-216
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-216
PRIOR PILING DATE: 2000-01-216
                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
US20020061569A1
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                                                                                      1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
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                                                                                                                                                                 GATTICIATGATCAGIATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC
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              Score 911.4; DB 10;
Pred. No. 8.9e-280;
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Best Local Similarity 99.3%;
Matches 915; Conservative
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Best Local Similarity 61.3%;
Matches 555; Conservative ; NAME/KEY: CDS ; LOCATION: (1)...(942) US-09-815-242-6823 376 427 음 ò

RESULT 2 US-09-815-242-6823 ; Sequence 6823, Application US/09815242

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                                                                                                                                                                                                                                                                                                                                                                                           Length 3656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                           37.0%; Score 340.4; DB 10;
larity 61.7%; Pred. No. 2e-97;
Conservative 1; Mismatches 343;
                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 577:
          TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                    301) 309-85
(301) 309-8512
                                                                                                                                                                 LENGTH: 3656 base pairs
                                                                   TELEFAX: (301) 309-851 INFORMATION FOR SEQ ID NO: 577: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
556; Conserv
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555
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A

FILING DATE: 04-May-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryiand COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 66/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 577, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Bexpression
FILE REFERRNCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.6e-54;
0; Mismatches 385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTCAGGGCTTGTGAAGAAAGTGAACC 868
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; ORGANISM: Bacillus licheniformis
US-09-974-300-1086
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Best Local Similarity 54.6%;
Matches 474; Conservative
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                                                                                                                                                                                                                                                                                    GENERAL LIVEXMALILUM:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PELING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2001-0-06
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
SPRIOR FILING DATE: 2001-10-06
SPRIOR FILING DATE: 2001-10-06
SPRIOR FILING DATE: 2001-10-06
SPRIOR FILING DATE: 2001-10-07
INUMBER OF SEQ ID NOS: 8481
SCOTTWARE: FREESEQ for Windows Version 4.0
LENGTH: 950
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                                                                                                                                                                                                                                 Sequence 1143, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
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Best Local Similarity 54.6%;
Matches 474; Conservative
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Best Local Similarity
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GGTTATGATTTACGTTATCTCATCGATACGG----AAGAAGACAAACTCAATCAGACCCGC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gringraciaecarariaganincaaaanacaanaaaniaariaaradaaaariceeeaaaaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATATGGAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TTAATGCAACAAGCTGTGCCTGAAGGCACTGGCGCAATGTATGCAATCATTGGTTTAGAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 GTAGAGGTCATTGAAGAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AATGAAGCAATTATTAATGCTTGCAAACAAGAGGAAGGGGAAGTCGTATCTGCGGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 AACTTTAACTCACCGGGTCAAGTAGTTATTGCGGGTGCGAAAGCTGCAGTTGAGCGTGCG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532 GTIGAACTITIGCAAGAAGCAGGIGCCAAACGCTIGAITCCTCTTAAGGIGTCAGGICCC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 TCTCACTGTGCATTAATGAAACCTGCAGCCGAGCAATTAGCGGTAACACTTGAGAATATT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 CANATIANTACACCANCANTATICGGTATTANATANCGTTGATGTGNANGCTGANACTGNA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGTTATGATTTATGGTATCTTGTTCAACAAGGTCCAGCTGAAGAACTTAATAAAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAG
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                                                                                                                                                                                                                                                                                                            1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCCAGTATCTAGGGATGGGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCATTATGTAAGAAGCAGGGCGAAACGTGCATTGCCGTTAGCTGTGACGTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 AACTATAACACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --AAGTITITICAGATITITACITIGICCCCTAGICGGCAAIACAGAAGCIGCIGIGAIGCAA
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                           Length 939;
                                                                                                                                                                                                                       Score 196.4; DB 10; Length
Pred. No. 6.7e-52;
0; Mismatches 386; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GICTIGICAGGITTIGITAAAAATIG 856
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             FastSEQ for Windows Version 4.0
                                                                                                influenzae
                                                                                                                                                                                                                         21.3%;
54.1%;
                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.1
Matches 470; Conservative
        SOFTWARE: FastSEQ for Win
SEQ ID NO 6878
LENGTH: 939
TYPE: DNA
ORGANISM: Haemophilus in
                                                                                                                                                            .. (939)
                                                                                                           FEATURE:

, NAME/KEY: CDS

, LOCATION: (1)...

US-09-815-242-6878
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301 GCCGGCGCCTTGTTTAAAGATGCGGTTTATGCCGTCAGAAAGCGCGGGAATTCATG 360
                                                                   GAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAG 417
                                                                                                           361 AATGAAGCCGTGCCGGCGGAGAAGGCGCGATGGCGGCCATTCTCGGCATGGACAGCCAG 420
                                                                                                                                                      GTCATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGA---GTGGTTACTCCAGCCAAC 474
                                                                                                                                                                                              GCGCTGAAAGAAGTGACGGACAAAATTTCCGAAGAAGGAAACCTTGTTCAGCTCGCCAAT 480
                                                                                                                                                                                                                                         TATAACACACTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTT 534
                                                                                                                                                                                                                                                                                      540
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                                                                                                                                                                                                                                                                                                                                                                    GAGCTTGCGAAAGAAAAGGCCGCAAAACGCCCGATTCCTCTCGAAGTCAGCGGGCCGTTC 600
                                                                                                                                                                                                                                                                                                                                                                                                            CACACCGCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTCTGAGCTGATGAGCCGGCAGCTGATAAGCTTCGTGAAGTTCTTGATGCGTGCACG 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 ATCAGCCGCCTGATTGACGAAGGCGTCACGACCTTCATTGAAATCGGTCCCGGAAAGGTT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGACATTAAGAATAAACTGATTGAACAGCTGTATTCCCCTGTACGCTTTGAAGAAACA
                                                                                                                                                                                                                                                                               TTGAACTGCCCTGGGCAAATCGTCATCTCGGGAACAGCTAAAGGCGTGGAGCTCGCTTCA
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: BLITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR PAPLICATION NUMBER: 60/191,078

PRIOR PELING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-28

PRIOR PILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
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Patent No. US20020061569A1
GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or c
NAME/KEY: misc_feature
LOCATION: (45732)...(45732)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (51602)..(51602)
DTHER INFORMATION: n equals a, t,
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a, t,
                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a, t
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LOCATION; (51786)..(51786)
OTHER INFORMATION: n equals a,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,
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LOCATION: (100091)..(100091)
DTHER INFORMATION: n equals a,
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,
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LOCATION: (117136)..(117136)
THER INFORMATION: n equals a,
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a,
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LOCATION: (80024)..(80024)
THEE INFORMATION: n equals a,
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a,
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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a,
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LOCATION: (653]3) ..(65313)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51805)..(51805)
OTHER_INFORMATION: n equals
                                                                                                                          APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nuclectide Sequence of the Haemophilus influenzae Rd Genome, Frag
FILE DE INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186F1
CURENT PAPLICATION WUMBER: US/10/329,960
PRIOR PILING DATE: 2003-01-02
PRIOR PILING DATE: 2000-08-23
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
LENGTH: 1830121
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a, t, g
                                                           Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
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LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals a,
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,
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LOCATION: (4747):.(4747)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (36636).
OTHER INFORMATION: n equals a,
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NAME/KRY: misc_feature
LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (44416)..(44
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LOCATION: (44975)..(44)
              RESULT 7
US-10-329-960-1/c
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172267 TITCCTCAATTAAACCAGAAGTGATGGCAGGTCATAGCTTAGGTGAGTATTCTGCGTTA 172208
          172387 GGTTATGATTTATGGTATCTTGTTCAACAAGGTCCAGCTGAAGAACTTAATAAAACTTGG 172328
                                                                                     172327 caaacrcagcccgcacrirriagcrgcricagrcgcrafrrarcgcgrarggaaagaaa 172268
                                                                                                                                                                                                                                                    172207 GTTTGTGCTGGCGTGTTGGATTTCCAAGATGCGATTAAATTAGTGGAATTTGCGCGGAAAA 172148
                                                                                                                                                                                                                                                                                                                                 172147 TTAATGCAACAGCTGTGCCTGAAGGCACTGGCGCAATGTATGCAATCATTGGTTTAGAT 172088
                                                                                                                                                                                                                                                                                                                                                                                                                172087 AATGAAĞCAATTATTAATĞCTTĞCAAAÇAAĞCAGAGĞAAĞGCGAAĞTCGTATÇTĞÇĞĞTĞ 172028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708
                                                                                                                                                                                                             292 GTGGCAAGCGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                           531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    828
                                                   TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAG
                                                                                                                              GGCTATC-----AGCCTGATATGGTTGCTGGTTTGTCTTGGAGAATACTCTGGCCTTG
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                                                                                                                                                                                                                                                                                                                                                                          412 GTAGAGGTCATTGAAGAAGCCTGTCAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCC
                                                                                                                                                                                                                                                                                             352 TATATGGAAGAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 AACTATAACACACACACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 GITGAACTITIGCAAGAAGCAGGTGCCAAACGCTIGATICCTCTIAAGGTGTCAGGTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171847 CAAATTAATACACCAACAATATCGGTATTAAATAACGTTGATGTGAAAGCTGAAACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  769 AGTATTGGGGTCATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 TITCACACCGCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 -- AAGTITITCAGATITIACTIGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yanamoto, Robert T.

APPLICANT: Yanamoto, Robert T.

IIILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKARYOUSE
FILE REPRENCE: ELITRA.011A
FURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6028, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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Pred. No. 7.5e-50;
0; Mismatches 386; Indels
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                                                                               NAME/KEY: misc feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a,
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                    ON: (122336)..(122336)
INFORMATION: n equals a,
                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                          EY: misc_feature
ON: (139910)..(139910)
INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.1%;
Matches 470; Conservative
CEY: misc_feature
ION: (121344)..(121344)
INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
                                                                                                                                                                misc feature (122336)..(12
                                                                                                                                                                                                                                                                                                                             misc feature (131360)..(13
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LOCATION: (142750)..(14
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LOCATION: (145942)..(1.
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Sequence 458, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT Charles A. Kunsch
APPLICANT Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faccialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 98.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                          781 GTTGAGTACATGGCGAGGGCGTAGAACATCTCTATGAAGTCGGCCCGGGCAAAGTG 840
                                                                                                                                             772 ATTGGGGTCATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTC
                           721 GATGCCATCCGTGACGCACTGGTACGTCAGTTATAACCCGGTTCAGTGGACGAAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM, MSDOS version 6.2 SOFTWARE: AGCII Text SOFTWARE: AGCII Text APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A FILING DATE: 04 May-2000 CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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.larity 58.6%; Pred. No. 3.7e-39;
Conservative 4; Mismatches 184;
                                                                                                                                                                                                                                                                          832 TTGTCAGGTTTTGTTAAAAAATTGATCAAAC 863
                                                                                                                                                                                                                                                                                                                                       841 ciracrédecreaceaacearrieresacae 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 458: US-09-070-927A-458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (301) 309-8512
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 458 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
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COUNTRY: USA
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US-09-070-927A-458
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ATGCAAGAAGCCGTACCGGAAGGCACGGGCGCTATGGCGGCAATCATCGGTCTGGATGAT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 185.6; DB 10;
Pred. No. 1.8e-48;
0; Mismatches 399;
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSED for Windows Version 4.0
SEQ ID NO 6028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 53.2%;
Matches 464; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(930)
US-09:815-242-6028
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LOCATION: (1).
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                                                                302 GTAAGTCCCTTACATTTGAAGATGCGGTCACACTTGTTCATCAACGGGGGACACTCATGG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 TGAATTGTCCAGGGCAAATTGTCCTGTCAGGGACTGCGAAAGGAATTGAACAAGCAGCAG
      GCGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGG
                                                                                                                                 AAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGG
                                                                                                                                                                                           419 TCATTGAAGAA---GCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACT
                                                                                                                                                                                                                                                                                                                                                                                       476 ATAACACACTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTG
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                                                                                                                                                                                                                                                                                                                      422 AGCTTGÁGGÁÁGTGGCTTCCGÁÁATTGCAGCGGÁCGGCGAÁGTTGCTGAACTTGCCAÁTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536 AACTITIGCAAGAAGCAGGIGCCAAACGCIIGAIICCICIIAAGGI 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 TATTAGCAAACAAAAGGGCCCAAGCGTGTCTTGCCACTTGCCGT 587
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APPLICANT: Chisen, Kari L.
APPLICANT: 29skind, Judith W.
APPLICANT: 29skind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 1000-101-101
TITLE OF INVENTION: MADER: US/09/815,242
CURRENT PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-12-7
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8032, Application US/09815242 Patent No. US2020061569A1 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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ORGANISM: Staphylococcus aureus
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Best Local Similarity 49.2
Matches 456; Conservative
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US-09-815-242-8032
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                                                                                                                                                                                                                                                      699 TGTGATGCAAAAAGAGGACATTGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCG 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 ACCGGGGAAAGTCTTGTCAGGTTTTGTTAAAAATTGATCAAACTGCTCACTTAGCTCA 878
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                                                             292 TGTGAGTGGCCCTTTCCATACGGCGCTGTTACAACCAGCATCAAAAAATTGGCTCAGGA 351
                                                                                                                                                                                                                                                                                                                   112 AATTATGCCCCAAGAGCCAATTCAAGCGTTATTGGAAAAGCAAGTCATGTCTGCGGTACG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 TCCAGGGAAAACATTAACTGGTTTTGTTAAAAAAATTGACAAAACAATTGAAATGCACCG 591
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GGTGTCAGGTCCCTTTCACACCGCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1D Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PELLORATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 00/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO SSS2
LEAGUES FASTERE FASTERE FOR WINDOWS Version 4.0
SEQ ID NO SSS2
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Pred. No. 6.3e-34;
0; Mismatches 259; Indels
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/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
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Conservative
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US-09-974-300-5552
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US-09-974-300-5552
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Indels
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Profarryoses
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/103-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-10-2-16
NUMBER OF SEQ ID NOS: 14110
SEC TAMES PRICES PRICES FREIGH WINDOWN VERSION 4.0
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Pred. No. 5.5e-30;
0; Mismatches 429;
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ilarity 49.8%;
Conservative
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Best Local Similarity
Matches 440; Conserv
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LENGTH: 906
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         GAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAG 417
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                                                     GATTTATATATACAACAACGATCAAGCAACTGAAATTTTAACTTCAGCAGCAAACACGTTA
                                                                                                  GGTTATGATTTACGTTATCTCATCGATACGGAAGAA---CAAACTCAATCAGACCCGC
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, Grant J.
APPLICANT: Yammanoto. Robert T.
APPLICANT: Yammanoto. Robert T.
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GATITICIATGATCAGIATCCGATTGTCAAAGAACGATTGATCGAGCGAGTCAGGTGCTC 120 120 357 417 474 534 295 gcrgacgrarrancarrigaagargcagrraaaarrgragaaaagrggrgarraarg 354 ececaaecarricciacregreradaaecareecrecadrarreecerragarrirear 414 GTCATTGAAGAAGCCTGTCA---AAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAAC 474 TATAACACACCTGCACAAATCGTCATTGCTGGAGAGTGGTTGCAGTTGATCGAGCGGTT 534 GAAAAAGGIAAATCATTAGGTGCAAAACGTGTCATGCCTTTAGCAGTATCTGGCCCATTC 594 CACACCGCTCTCCTTGAGCCTGCTAGCCAGAACTAGCTGAAACTCTAGCTCAGGTAAGT 654 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGA---CAAACTCAATCAGACCCGC 121 GACTTTGATATTTTAGAGACAATGTTTAGTGAAGGGGGAAAATTGGGTGAAAATTGGGTGAAA TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAG 181 AACACGCAACCAGCTTTATTGACGCATAGCTCGGCGTTA-----TTAGCGGCGCTAAAA GGCTATCAGCCTGATATGGTTGCTGGTTTGTCTTGGAGAATACTCTGCCTTGGTGGCA ATTAATTGCCCAGGTCAAATTGTTGTTTCAGGTCACAAAGCTTTAATTGATGAGCTAGTA GAACTITIGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTT 1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 1 Arcagradadacacantrarritrecegacaaggrececaaaagrregrafegeacaa GATTTATATAACAACAACGATCAAGCAACTGAAATTTTAACTTCAGCAGCAAACACGTTA GAAGAAGCGGCTCCTGCTCTCTCGCCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAG 298 AGCGGCGCCTTGGATTTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATG 415 AAAGTCGATGAAATTTGTAAGTCATTATCATCTGATGACAAAATAATTGAACCAGCAAAC AATTTGAATCCCGATTTTACTATGGGGCATAGTTTAGGTGAATATTCAAGTTTAGTTGCA 15; Length 906; 535 ò d

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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                         190 GCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGCTAT---CAG
                                                                                                                                                                                                                                                                                                                                                                                            247 CCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGCGGCGCC
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                76 CAGCAGGCGCTGGTGCGCGATACCTTCGCCGAGGCCTCCGAGGCGCGCTCGGTTACGACCTT
                                                                                          CGTTATCTCATCGATACGG----AAGAGACAAACTCAATCAGACCCGCTATACGCAACCA
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OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII TEXT
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MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STATE: Ma
COUNTRY:
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ATTGGGGTCATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTC 831
                                                                                                                  TITICAGAITITACTIGICCCCTAGICGCAATACAGAAGCT----GCTGTGAIGCAAAA 711
                                                                                                                                                                                                                                                                                                                                               715 GAAGTAATTAAATCTAATATGGTCAAACAATTATTATTCACCAGTACAATTCATTAACTCA 774
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                                                                                                                                                                                                                                                                          GAGGACATTGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTTCGTATGAAAGT
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Pred. No. 8.3e-28;
0; Mismatches 417; Indels
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APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7796
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-22-27
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Patent No. US20020061569A1
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ORGANISM: Pseudomonas aeruginosa
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Best Local Similarity 49.0
Matches 410; Conservative
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; LOCATION: (1)...(939)
US-09-815-242-7796
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GENERAL INFORMATION:
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                                                                                           ATTGGGGTCATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTC
                                                                                                                                1160 ACAGAATGGCTAATAGACCAAGGTGTTGATCATTTTATTGAAATTGGTCCTGGAAAAGTT
                                                                                                                                                                             832 ITGICAGGITITIGITAAAAAATIGAICAAACIGCICACTIAGCICAIGIGGAAGAICAA
                                                                                                                                                                                                                       4220 TTATCTGGCTTAATTAAAAATAAATAGGGATGTTAAGTTAACATCAATTCAAACTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Macar, James G
APPLICANT: Macar, James G
APPLICANT: Facciotti, Daniel
TITLE OF INVENTION: SCHIZOCHTRIUM PKS GENES
FILE REFERENCE: CGNE.131.02US
CURRENT APPLICATION NUMBER: US/10/331,061
CURRENT APPLICATION NUMBER: US/09/231,899
PRIOR APPLICATION NUMBER: US/09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                              4280 GAAGATGTGAAAGGATGGAATGAAA 4305
                                                                                                                                                                                                                                                                 GCGAGITIAGIAGCACTITIAGAAAA 917
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 77, Application US/10331061; Publication No. US20030101486A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%;
Best Local Similarity 46.8%;
Matches 332; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Vibrio marinus
US-10-331-061-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118.4; DB 7;
Pred. No. 1.6e-26;
0; Mismatches 461;
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-85.12
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
TENTY: (5251 base, pairs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%;
48.6%;
                                                                                                                                                                                                                                                                                                                            LENGTH: 6251 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity 48.6
Matches 450; Conservative
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US-08-781-986A~25
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572 CICTIPAAGGIGICAGGICCCITICACACGGCICTCCTTGAGGCCTGCTAGCCAGAAACTAG 631
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Search completed: June 11, 2003, 20:01:40 Job time: 171 secs

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GenCore (c) 1993 -	ı	score:	Scoring table: IDENTITY_NUC Gapop 10-0 , Gapext 1.0 Searched: 16154066 seqs, 8097743376 residues	umber o	angth: 0 angth: 20000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	īΛ	4: em estmi.* 5: em estpl:* 7: em estpl:* 8: em lestpl:*		14: gb_ests:* 15: em_estfun:* 16: em_estcom:* 17: gb_gss:* 18: em_gss_hum:*	em_gss_pir em_gss_tur em_gss_fur em_gss_mam em_gss_mus em_gss_mus	26: em_gss_pro:* 27: em_gss_rod:* No. is the number of results predicted by chance to have	n or equal to , analysis of	o Descripti	C 1 95.6 10.4 1237 17 AP029428 C 2 87.6 9.5 511 14 BQ818656 C 3 82.2 8.9 544 9 AU0.69821 C 4 53.2 5.8 77 17 AZ049336 C 5 53 5.8 78 11 BP712296 C 5 52.6 5.7 491 12 BP512296

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Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii

Chlamydomonadacae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadacae; Chlamydomonas.

E 1 (Dases 1 to 511)

S Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre

,P., McDermott,J.P., Shager,J., Silflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1030

L Contact: Charles Hauser

DCMS Box 91000

DCMS LOX 91000

DUMS University
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                                                                                                                                                                                                                                                    GAGATGGCGGCAAATTACCCTATCGTAGAAGAACGTTTGCTGAAGCTTCTGCGGCTCTG 279
                                                                                                                                                                                                                                                                                                                    GGTTATGATTTACGTTATCTCATCGATACGGA---AGAAGACAAACTCAATCAGACCCGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                      CAGACGCAGCGGCGTTATTAACCGCTTCCGNTSCGMTWTGGCGCRTTTGGCAGCAGCAG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 TGMGCTGGCGTCATCAACTTTGCTGATGCCGTTCGTCGGTGGAAATGCGGCGGTAAATTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ818656
1030072D02.yl C. reinhardtii CC-1690, Deflagellation (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                 a typhimurium LT2, Lambda DASH II"
DASH II; sequenced using Li-Cor
                                                                                                                                                                                    1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
                                                                                                                                                                                                                                                                                                                                                                                      TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAG
                                                                                                                                                     Gaps
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9
                                                                                                                  Length 1237;
                                                                   14 others
                                                                                                                                                     Indels
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db xref="taxon:3055"

/clone_lib="C. reinhardtii CC-1690, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGAAGAGCGGCTCCTGCTGACTCTGGCAAGATGG 391
                                                                                                                Score 95.6; DB 17;
Pred. No. 1.1e-17;
7; Mismatches 167;
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                                                                   281
/clone="1257-T7"
/clone_lib="Salmonella
/note="Vector: Lambda_D
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                                                                   304
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Tel: 919 613 8159
Fax: 919 613 8177
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ilarity 54.7%;
Conservative
                                                 sequencer"
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                                                                                                                Query Match
Best Local Similarity
Matches 217; Conserv
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/note="Vector: pBluescript II SR-; Site_I: EccRI; Site_2:
XhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap_II
(Stratagene) in the EccRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU069821 Rice panicle at flowering stage Oryza sativa (japonica cultivar-group) cDNA clone B3726_7A, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sprantoophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatoophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae.
Enrhartoideae; Oryzae.
I (base 1 to 544)
Sasaki, T. and Yamamoto, K.
Rice cDNA from panicle at flowering stage
Uppublished (1996)
Contact: Takuj; Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTIGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 87.6; DB 14;
Pred. No. 1.7e-15;
0; Mismatches 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.3%;
Matches 229; Conservative (
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25 (1712)

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/db.xref="caxon:235"
/db.xref="taxon:235"
/clone="bc7"
/clone="bc7"
/clone="bc7"
/clone="Vector: pBluescript SK(-) (STRATAGENE); Genomic DNA was mechanically sheared, blunt ended, and size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 Kb were recovered and ligated to the EcoRV site of the pBluescript SK (-) vector:"
115.0 g 74 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ796704 1inear EST 30-JUL-2002 EST 5642 Ripening Grape berries Lambda Zap II Library Vitis vinifera cDNA clone RT051B09 3', mRNA sequence.
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Vitis vinifera.
Vitis vinifera.
Vitis vinifera.
Vitis viniferaliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
                            1 (bases 1 to 427)
Sanchez, D.O., Zandomeni, R.O., Cravero, S., Verdun, R.E., Pierrou, E. Sanchez, D.O., Zandomeni, R.O., Cravero, S., Aquero, F., Frasch, A.C.C., Andersson, S.G.E., Rosetti, O.L., Grau, O. and Ugalde, R.A. Gene discovery through genomic sequencing of Brucella abortus Infect. Immun. 69 (2), 865-868 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 GAAGAIGCGGTIGCTIGGTAGCCTAAGCGTGGAGCCTAIAIGGAAGAGCGGCTCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 GCCGACACGGCGCGCTCTCTCGCCATTCGCGGCAATGCCATGCAGAGGCGGTTCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 GACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAAGAAGCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 GTTGCTGGTTTGTCTTGGAGAATACTCTGCCTTGGTGGCAAGCGGCGCCCTTGGATTTT
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                                                                                                                                                                                                         21101004
Contact: Zandomeni, R.
Contact: Zandomeni, R.
Contro Asconatigacion en Ciencias Agropecuarias (CICA)
Instituto Nacional de Tecnologia Agropecuaria (INTA) C.C.
Castelar. Buenos Aires, Argentina
Tel: 5411-4621-3316/1683
Fax: 5411-4621-3316
Fax: Sandomeni@inta.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Brucella melitensis biovar Abortus"
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llarity 48.1%; Pred. No. 6e-05;
Conservative 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: shotgun.
Location/Qualifiers
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AZ049336.1 GI:7273251
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
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Brucella melitensis biovar Abortus
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
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/dev_stage="flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at
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cultiva="Nipponbare"
/db xref="taxon:39947"
/clone="E3726_7A"
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Hamdis, Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (akin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-90-61-28-67
Email: romieu@ensm.inra.fr
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Pred. No. 0.0001;
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polylinker; Site 1: Not 1; Site 2: Eco RI; NoT CGAP_Sub7
is a subtracted Tibrary derived_from NCI CGAP_Sub6. The
NCI CGAP_Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising; the IMAGE pool (NCI CGAP_Sub6 was used
as tracer in a subtractive hybridization with a driver
comprising; the IMAGE pool (NCI CGAP_Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising; the IMAGE pool (NCI CGAP_Sub6) in LLAM
3334.3337, 3682-3683, 3798-3803, [445608-145675, 1500552-1502855);
NCI CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3752, 3776-3778
(IMAGE CloneIDS 1252912-1325831, 1471368-1472903,
1492104-1493255); NCI CGAP_Eu5 pool 1 LLAM 3575-3582,
3851-3854 [IMAGE CloneIDS 1257096-1258631,1466064-147098]
; NCI CGAP_GCA pool 1 LLAM 3164-3167, 3116-3720,
1101192-1101959, 1217928-1220615; NCI CGAP_COLO pool 1
LLAM 2644-2653, 2062-3068 [MAGE CloneIDS 985608-986759,
1101192-1101959, 1217928-1220615; NCI CGAP_Sub3 [IMAGE
CloneIDS 27708616-2710535] and NCI CGAP_Sub3 [IMAGE
CloneIDS 2708616-2710535] and NCI CGAP_Sub3 (IMAGE
CloneIDS 2712456-273591) (10% of the driver population),
plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE
CloneIDS 2723522-2739326) (40% of the driver population),
plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE
CloneIDS 2723522-2733291) (40% of the driver population),
plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE
CloneIDS 272456-2733591) (40% of the driver population),
plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE
CloneIDS 272456-2733591) (40% of the driver population),
subtraction was performed as previously described [Bonaldon).
TWO Approaches TO Redilitate Gene Discovery. Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbs-r@mail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNI at:
Seq primer: M13 Forward
HE512296 491 bp mRNA linear EST 07-DEC-2000 UI-H-BW1-amb-e-04-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone INAGE:3069391 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 491) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Pred. No. 0.0001;
0; Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.6%;
Matches 127; Conservative
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BJ372892 BJ372892 414 bp mRNA linear EST 08-MAR-2002 BJ372892 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc14f21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM277916 STP 20-DEC-2001 As type mRNA linear EST 20-DEC-2001 As tgz_50D12_SKPL Ascaris suum adult male testis germinal zone from Alan Scott Ascaris suum cDNA clone As_tgz_50D12_5', mRNA sequence.
                                        545 CTGGCATTTACAGGAGCTTTCAGTTTTGAGGATGGGCTTAAGCTGGTTAAGCTTAGAGGA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 crencerciarecrerecentracecriciaerrecaerreraciaerrecaecrerecae 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Mycetozoa; Dictyosteliida, Dictyostelium.

(Dasses 1 to 414)
Urushihara,H. Tanaka,Y., Kohara,Y. and Shin i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
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                                                                                                              349 GCCTATATGGAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tahini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                            Query Match

4.6%; Score 42.6; DB 13;
Best Local Similarity 48.1%; Pred. No. 0.11;
Matches 117; Conservative 0; Mismatches 126;
dev_stage="Culmination stage"
42 c 152 g 116 t
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BJ372892.1 GI:19282275
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BM277916/c
                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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AUTHORS
TITLE
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BJ372892
LOCUS
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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EST495727 cSTS Solanum tuberosum cDNA clone cSTS16L11 5' sequence,
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1 (bases 1 to 744)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bedgil, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes
                TIGGAGIGGITACTCCAGCCAACTATAACACCCTGCACAAATGGTCATTGCTGGAGAAG 511
                                                                                                                                                                                                                                                                                                                               CTCTTAAGGTGTCAGGTCCCTTTCACACGGCTTCTCTTGAGCCTGCTAGCCAGAAACTAG 631
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1.800-711-6195, email cdna@resgen.com
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/organism="Solanum tuberosum"
/oultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS16L11"
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                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris.; Losses 1 to 501)
Blaxter, M.L., Parkinson, J., Whitton, C., Daub, J., Guiliano, D., Hall, N., Quayle, M. and Barrell, B.
Edinburgh University/Sanger Centre Nematode EST Project
Unpublished (2000).
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//dev_srage="Adult"

//note="Vector: Lambda Zap II, Site 1: EcoRI; Site 2: XhoI;

Library was made from dissected testis germinal zone from adult male Ascaris suum collected from abbatolis.

Constructed by Michelle Lizotte-Waniewski for Alan Scott,

Johns Hopkins University Medical School, Baltimore, MD."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:6253"
/clone="As_tgz_50D12"
/clone lib="Ascaris suum adult male testis germinal zone
from Alan Scott"
                                                                                                                                                                                                                                                              Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The library was prepared by Michelle Lizotte-Waniewski for Alan
Scott, Johns Hopkins University Medical School, Baltimore.
Sequencing was performed by the Pathogen Sequencing Unit, Sanger
PCR PRimers
PCR PRimers
PCR PRIMERS
PROWARD: T3
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University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh,
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Seg primer: SXPL
High quality sequence stop: 446.
Location/Qualifiers
BM277916
BM277916.1 GI:17971174
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                                                                                                                                                                                                                   Contact: Blaxter ML
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277853 556 bp mRNA linear EST 20-DEC-2001 tgz_49E05_SKPL Ascaris suum adult male testis germinal zone from a Scott Ascaris suum cDNA clone As_tgz_49E05 5', mRNA sequence.
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1 (bases 1 to 556)
Blaxter,M.L., Parkinson,J., Whitton,C., Daub,J., Guiliano,D., Hall
A., Quayle,M. and Barrell,B.
Edinburgh University/Sanger Centre Nematode EST Project
Unpublished (2000)
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Fax: +44 131 670 5450

Faxi: +44 131 670 5450

The library was prepared by Michelle Lizotte-Waniewski for Alan Scott, Johns Hopkins University Medical School, Baltimore. Sequencing was performed by the Pathogen Sequencing Unit, Sanger Centre, Cambridge, UK (Neil Hall, Mike Quail & Bart Barrell). The Sequence contained a Polya tail (trimmed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testis germinal zone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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/db_xref="taxon:6253"
/clone="As tgz_49E05"
/clone lib="Ascaris suum adult male
from Alan Scott"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.6%; Score 42.6; DB 13;
Best Local Similarity 48.2%; Pred. No. 0.13;
Matches 120; Conservative 0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542.
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Plate: 49 row: B column: 05
Seg primer: SKPL
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Location/Qualifiers
1. .556
                                                                                                                                                                                                                  BM277853.1 GI:17971111
                                                                                                                                                                                                                                                                                                                           pig roundworm.
Ascaris suum
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AAGCAGGTG 556

548

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/Anotal-More and an analysis of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
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EST439657 potato leaves and petioles Solanum tuberosum cDNA clone cSTB39921 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                              Contact: TIGR
The Institute for Genomic Research
Rockville, 10550, USA
Tel: (301)838-0200
Email: http://www.tigr.org/tdb/potato/
For clone information, please contact Research Genetics, Libraries Division, tel# 1-800-711-6195, email- cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solatum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 523)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterida I; Solanales, Solanacese; Solanum.

1 (bases 1 to 435)

van der Hoven, X., Bezzerides, J., Bachem, C., Horvath, B., Visser, R. Holt, I.E., Liang, F., Hansen, T.S., Utterback, T., Bowman, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Tanksley, S.D. and Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CTGGCATTTACAGGAGCTTTCAGTTTTGAGGATGGGCTTAAAGCTGGTTAAGCTTTAGAGGA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4113"
/clone="cSTA45G17"
/clone=lib="potato stolon, Cornell University"
/tissue_type="axillary buds of stem explants, swelling stolons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 TTGGTGGCAAGCGGCGTTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 CAAGAAAAGGGCTATCAGCCTGATATGCTTGCTGGTTTGTCTCTTGGAGAATACTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 CAACAAATTGATTCGGTTGATGTCACATGTGGCTCTGAGCTTGGGCGAATACACTGCT
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Pred. No. 0.13;
0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 GCCTATATGGAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GAAGCTATGCAGGATGCTGCTGCTGCAAAAGTGCAATGGT 311
                                                                                                                                                                                                                                                                      Generation of ESTs from potato swelling stolons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Solanum tuberosum"
oultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="1 to 3 days"
/lab_host="SOLR"
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53.7%;
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Best Local Similarity 53./v,
Local Similarity 53./v,
Conservative
                                                                                                                                                                                                                                                                                               Unpublished (1999)
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ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                       BE919981
EST423750 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB3E24 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFIEBSSE4 101-NOV-2000 EST444851 potato stolon, Cornell University Solanum tuberosum cDNA Clone cSTA45G17 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and perioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
I (bases I to 33)
van der Heeven,R.S.
Bezzeridae,J., Holt,I.E., Liang,F., Cho,J.,
Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 CAAGAAAAGGGCTATCAGCCTGATATGGTTGCTTGTTGTTTGGAGAATACTCTGCC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 CAACAAATAATTGATTCGGTTGATGTCACATGTGGTCTGAGCTTGGGCGAATACACTGCT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 TIGGIGGCAAGCGGCGCCTIGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 criedcartracaddadcrrrcagrirridaddardddcrrraagcricarraagcrraadda 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 GCCTATATGGAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGT 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4113"
/clone="cSTB3E24"
/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .373
/organism="Solanum tuberosum"
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Solanum tuberosum
|| ||
131 TTGCTATTG 123
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International Triticeae EST Cooperative (ITEC)
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Eukaryora, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;

Bukaryora, Viridiplantae, Streptophyta, Embryophyta; Pooleae

; Triticeae, Triticum;

; Thiticeae, Triticum;

; Thiticeae, Triticum;

; Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier

; S., Dubcoveky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,

Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Jodinier,P.,

Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,

Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,

Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/cultivar="Kennebec"
/cultivar="Annebec"
/dxxef="Laxon:4113"
/clone="CSTB39P2"
/clone="CSTB39P2"
/clone="CSTB39P2"
/clone="Ib="potato leaves and petioles"
/clone="Ib="potato leaves and petioles"
/clone="Ib="potato leaves"
/clone="Ib="potato leaves"
/clone="Ib="potato leaves"
/clone="Bayes"

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PSR6966 ITEC PSR Wheat Pericarp/Teeta Library Triticum aestivum
DE427401
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Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning , C.M., Fry, W.E., Tanksley, S.D. and Baker, B. Generation of ESTS from potato leaves and petioles Unpublished (2000) (Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 CAAGAAAAGGGCTATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CAACAAATAATTGATTGGTTGATGTCACATGTGGTCTGAGCTTGGGGCGAATACACTGCT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TTGGTGGCAAGCGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.4; DB 12;
Pred. No. 0.14;
0; Mismatches 76;
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Norfolk, Norwich MR4 7UH UNITED KINGDOM
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
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Best Local Similarity 53.7%;
Matches 88; Conservative
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                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramarsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length obba libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATTGCAAGAAAAGGGCTATCAGCCTGATAIGGTTGCTGGTTTGTCTCTTGGAGAATAC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 AATACGCCAGTAGAGGTCATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTT 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 CGTGGAGCCTATATGGAAGAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                               / Organism="Triticum aestivum"
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/ tissue type="pericary/testa"
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/ note="vector: Lambda ZAP II (Stratagene)"
a 195 c 83 g 124 t 21 others
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HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 6 days neonate skin cDNA to
clone_lib:RIKEN full-length enriched mouse cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 650;
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Pred. No. 0.17;
0; Mismatches 184;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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http://wheat.pw.usda.gov/genome_
Location/Qualifiers
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 45.1
Matches 151; Conservative
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TITLE

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Query Match

4.6%; Score 42.4; DB 11; Length
Best Local Similarity 47.4%; Pred. No. 0.19;
Matches 127; Conservative 0; Mismatches 141; Indels
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                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="evidence:NAS
hypothetical protein
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he : 1428 secs
                                                                                                                                                           Location/Qualifiers
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196 c 222 g
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S Adachi, J., Alamawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imochani, K., Itoh, M., Izawa, M., Kasuka, T., Kojina, Y., Itoh, M., Izawa, M., Kayai, S., Kavai, J., Kojina, Y., Konno, H., Kouda, M., Kayai, K., Numazaki, R., Numazaki, R., Nomura, K., Numazaki, R., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Sakai, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Shibata, Y., Shinagawa, A., Shiraki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yashida, K., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kando, M., Adachi, J., Fukuda, S., Alzawa, K., Isawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Cokazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaagterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nixaido, I., Pasole, G., Caravant, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M., Jull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Mantaker, C., Wilming, L., Wynshaw-Boris, A., Wentz, C., Whittaker, C., Wilming, L., Wantaki, Y., Furuncionalla and Haysphizaki, Y.
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Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                          Konno, H., Atiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikagami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warshiwagi, K., Ordeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Marsuura, S., Kawai, J. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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COMMENT

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